AAW14925 standard; Protein; 467 AA.

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61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PGKGLEWIGYIYGSGGGTNYNFSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCA--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RPDCTTICYGGWYDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 ---SNILKYLHWLLYWGQGVLVIVSSASIKGPSVFPLAPCSRSISESTAALGCLVKDYFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCSVSGGSISGDYYWFWIRQS 60
                                                                                                                                                                                                                                                                                                                                     regions of human gamma-4, gamma-4E carrying an L236E mutation in The hinge region, and gamma-4PE carrying and E236E and 8229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies e.g. CE9 gamma-4P. CE9 gamma-4E and CE9 gamma-4PE, in which the human 1964 Fe binding domain framework is combined with the antigen binding domain season AMM14922-23) of macaque antibuman CP4 monoclonal antibody E9.1. These antibodies show high and show reduced or absence of effector function. The gamma-8E and show reduced or absence of effector function. The gamma-8E and eppleating activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 467;
                                                                                                                                                                                            Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                      Polypeptides (AAW14925-27) respectively comprise the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.0%; Score 2112.5; DB 18
84.5%; Pred. No. 7.8e-119;
Live 24; Mismatches 41;
                                                                                                                                                                                                                                                                                      Claim 6; Page 91-93; 155pp; English.
                                                                                                        Hanna N, Newman RA, Reff ME;
96WO-US14324
                                   95US-0523894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 402; Conservative
                                                                  (IDEC-) IDEC PHARM CORP
                                                                                                                                         WPI; 1997-201913/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 AA;
                                                                                                                                                           N-PSDB; AAT62870
 05-SEP-1996;
                                   06-SEP-1995;
                                                                                                                                                                                                                                                   arthritis
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61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTKTYTCNVDHKPSNTKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
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                                                                                                                                  CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cypomolgue monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4. gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and 5229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 1964 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque antihuman CD4 monoclonal antibody E9.1. These antibodies show high and show reduced or absence of Effector function. They can be used to treat autoimmune diseases such as rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
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84.5%; Pred. No. 8.9e-119;
tive 24; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 82-84; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       Reff ME;
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                                                                                                   Human gamma-4 heavy chain.
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanna N, Newman RA,
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                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 05-SEP-1996;
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                                                                   18-OCT-1997
                                                                                                                                                                                                                                                                                                 13-MAR-1997.
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                               178 YFFEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN 237
                                        168 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSN 227
                                                                                    TKVDKTVERKCCVE---CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 283
                                                                                                                         TKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 297
                                                                                                               EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
                                                                                                                                                      PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPE 417
                                                                                                                                                                404 NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 462
                                                                                                                                                                                             NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of the reshaped CAMPATH-1 heavy chain antibody
                                                                                                                                                                                                                                                                                                                                                Antigen, CDR, complementarity determining region, graft rejection, autoimmune diseases, rheumatoid arthritis, allergy.
------GGAVAAFDYWGQGTLVIVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanisation of antibodies binding to human CD4 antigen - by mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Complementarity determining region 1"
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                                                                                                                                                                                                                                                                                                                             Reshaped CAMPATH-1 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorman S D,
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                 AAR22757 standard; Protein; 470 AA
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                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ23570.
                                                                                                                                                                                                                                                                                                                                                                               Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 425
Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatcid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to alleviate allergies. Tolerance to allergens could also be achieved. See also AAR22754-R22763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; vynomolgue monkey; autoimmune dieeses; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host dieease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4PE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 TICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 -----FDYWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                                                                                                                                                                                                                  Length 470;
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                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           82.3%; Score 2122; DB 13;
86.6%; Pred. No. 2.1e-119;
tive 13; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW14927 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gamma-4PE heavy chain.
                                                                                                                                                                                                                                                                                                                                                                 Matches 408; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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368 AKGQPREPQUYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 427
                                                                                                                                                                                                                  AAB26884;
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                                                                   428
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                                                                                                                                               RESULT 11
AAB26884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 IGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTTI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 CYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 YHGDWFDPWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 NSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 VDGVEVHNAKTKPREEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LFLVATATGVHSQVQLQQWGAGLLKPSETLSLTCTVYGGSFSG-YYWSWIRQPPGKGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEW 67
                                                 signal peptide sequence encoded by
                                                                                                          /note= "human gamma 1 chain constant region and the variable region from anti-rhesus D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-32 KD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The human monoclonal antibody D7C2, of isotype IgM, recognises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.3%; Score 2223; DB 17; Length 472; 90.6%; Pred, No. 1.9e-125; ive 8; Mismatches 32; Indels 4.
                                                                                                                                                                                                                                                                                                                                                              Margaritte C;
                                                                 synthetic linker
               1. 19
/label= signal peptide
/note= "mouse VH signal
                                                                                                                                             antibody D7C2"
                                                                                                                                                                                                                                                                                                                                                           Chaabihi H, Edelman L, Kaczorek M,
                                                                                             heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 35-37; 46pp; French.
Location/Qualifiers
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PROTEINE PERFORMANCE.
                                                                                                                                                                                                                                               94FR-0010566
                                                                                                                                                                                                                                                                               94FR-0010566
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Best Local Similarity 90.67
Matches 425; Conservative
                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                              1996-162018/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT26889
                                                                                                                                                                                                                                                                             02-SEP-1994;
                                                                                                                                                                             FR2724182-A1
                                                                                                                                                                                                                                             02-SEP-1994;
                                                                                                                                                                                                                                                                                                             INSP ) INST
                                                                                                                                                                                                               08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
               Peptide
                                                                               Protein
                                                                                                                                                                                                                                                                                                                             (PROT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transformation of a hybridoma with a gene encoding an immunoglobulin heavy chain polypeptide for enhanced production of monoclonal antibody
364 AKGQPREPQVYTLPPSRDELIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RPDCTTICYGGWV---DVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSG-YYWTWIRQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.7%; Score 2131; DB 21; Length 462; ilarity 85.4%; Pred. No. 6e-120; Conservative 18; Mismatches 32; Indels 20;
                                                                                                             476
                                                                                                                                                         DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYIQKSLSLSPGK 472
                                                                                                             DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; immunoglobulin heavy chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunoglobulin heavy chain amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 40-43; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                       AAB26884 standard; Protein; 462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2000; 2000WO-JP02022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0087929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2001. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kusunoki C, Fukushima A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-611721/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA09695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200058499-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000.
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Matches 409;
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The sequences given in AAR93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kD antigen of human cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified using the sequences given in AAT18040-58. The monoclonal antibody may be used in the diagnosis of hCMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PPGKGLEWIGTIYYSG-STYYNPSLKSRVTISVDASNNQFSLKLSSVTAADTAVYYCAR- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKHLWFFLLLVAAPRWVLSQVKLQQWGGGLLQPSETLSRTCVVSGGSIS-GYYYWTWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGDSISRSSYSWGCIRQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TSPQYYDLLTGSPPSYWGQGTLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDKKVEPKSCDKTHICEPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 PRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYF
                                                                                                                    Human monoclonal antibody binds to cytomegalovirus 65 kD antigen produced by primer amplification, used in the diagnosis of hCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.6%; Score 2230.5; DB 17; Length 475; Best Local Similarity 89.7%; Pred. No. 6.8e-126; Matches 428; Conservative 11; Mismatches 35; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-rhesus D recombinant antibody D7C2 heavy chain.
                                                                                                                                                                                                                  Claim 4; Page 16-18; 22pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                      WPI; 1996-154852/16
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 475 AA;
       (TANA/) TANAKA H.
                                                                               N-PSDB; AAT18059
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                          60 PGKGLEWIGYIYTSG-STNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR-P 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 YFPEDVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGIQIYICNVNHKPSN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 TKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 297
                                                                                                                                                                                                                                                                                                                                                                                                                        121 RPDCTTICYGGWVDVW---GPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                232 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 PAPIEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPE 411
                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                              1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIRS-YYWNWIRLP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                      1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQCNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; amplify; PCR; light chain; MAb; 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation.
                                                                                                                                          87.8%; Score 2262; DB 21; Length 470; 90.4%; Pred. No. 8.7e-128; 1. Mismatches 23; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20..475
/note= "Mature heavy chain"
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                                                                                                                                                                                         Matches 433; Conservative
                                                                                                                                                                   Local Similarity
                                                                                                470 AA;
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                                                                                                  Sequence
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     number of human immune system associated proteins (HISAPB). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, sclerosis, myasthenia erythemmatosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
treatment; prevention; cell proliferation; immune system disorder.
                                                                                                                                                                            60 TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARG 119
                                                                                                                                                                                                                                                    238
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                                                                                                                                                                                                                         ---DDVGLRGGNYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 175
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                                                                                                                                                      PPEPVTVSWNSGALTSGVHTPPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                                                                                                                            PRPDCTTICYGGW-VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                                                                                                                                            APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                                                                                                                                                                                                                                             present invention provides the coding and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                    NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                              DB 22; Length 473;
                                                                                                                              7;
                                                                                                            88.4%; Score 2277.5; DB 22; Lengt 90.8%; Pred. No. 1e-128; ive 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
320
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/label= Signal_peptide
20..470
/label= Mature_ISMO-2
Claim 1; Column 53-56; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system molecule, ISMO-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44721 standard; Protein; 470 AA.
                                                                                                                   Best Local Similarity 90.8%
Matches 434; Conservative
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                                                                                           473 AA;
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Peptide
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Immune system molecules used in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation
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/note= "shows similarity to Ig superfamily protein
domain"
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                                                                 "Casein kinase II phosphorylation site"
                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Protein kinase C phosphorylation site"
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/note= "conserved Ig/MHC protein block"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 60-61; 69pp; English.
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N-PSDB; AAZ50012.
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Baughn MR;
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Gaps

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Length 476;

Score 2309, DB 23; Length Pred. No. 1.4e-130, 9; Mismatches 33; Indels

91.2%;

Query Match
Best Local Similarity 91.2'
Matches 434; Conservative

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241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360

DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP

241

181

301 301

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180

121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180

121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP

EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV

1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60

420

IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY

361

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Protein sequence of primatised form of the heavy chain of 16C10 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.
                                                             420
IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of monoclonal antibody which specifically binds to B7.1 antigen
                                                             361 IEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNY
                                                                                                                              KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                         AAU11646 standard, Protein, 476 AA
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Chimeric - Macaca sp.
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AAU1646
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New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
  361 IEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
                                                                                                                                                                                                             Human, immune system associated protein; HISAP-4; immune disorder; Infection; autoimmune disease; cancer.
                                       421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                  Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                  Corley NC, Guegler KJ,
                                                                                                                                                                                     Human immune system associated protein HISAP-4.
                                                                                                             AAB36206 standard; protein; 473 AA
                                                                                                                                                                                                                                                                                                                          98US-0049672.
                                                                                                                                                                                                                                                                                                                                                   98US-0049672
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Yue H, Lal P,
Hillman JL, Au-Young J;
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N-PSDB; AAC66522.
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                                                                                                                                                             15-FEB-2001
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD80) for inducting the apoptosis of B7.4 cCD80 and/or B7.2 antigen (CD80) for inducting the apoptosis of B7.4 cCD80. The invention is cuseful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymptora, B sells promote the growth and/or metastasis of tumours, cancer where B cells promote the growth and attribution as sells in inflammatory bile disease, altergy, multiple sclerosis. Crype I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, altergy, multiple sclerosis.

Cor graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food related allergies e.g. migraine, crhinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 16C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of

used in the inventic interleukin-2 (IL-2)

476 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                       2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01817-20). The primatised antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKHLWFFLLLUVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                 for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                 human B7.1 or B7.2 antigen
                                                                                                                                                                                                                                                                                                                                                                                Length 476;
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                                                                                                                                                                                                                                                                                                                                                                            89.6%; Score 2309; DB 18;
91.2%; Pred. No. 1.4e-130;
tive 9; Mismatches 33;
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               monoclonal antibody binding
                                                                         Claim 14; Fig 10B; 81pp; English
                                                                                                                                                                                                                                                                                                   and graft-versus-host disease.
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Best Local Similarity 91.2'
Matches 434; Conservative
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chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAb's) that bind selectively to B7.1 (CDB0) or to B7.2 (CDB6) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving CT cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type CT diabetes mellitus, theumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. CT diabetes mellitus, theumatory and multiple sclerosis, graft vs. CT diabetes mellitus, transmuch of arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. CT deficiency virus) or inflammatory disease and tumnouse. Optionally the MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAb's are optionally combined with other proteins cor small molecule immunosuppression, i.e. it inhibits induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and corrections antigen-specific immunosuppression, i.e. it inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a primatized form of the antibody 16C10 heavy
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                                                                                                                                                                                                                                                                                                                                             New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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                                                                                                                                                                                                                                              Hanna N;
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Macaca fascicularis.
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476 AA;
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                                                                                                        Matches 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD80) and or inducing the apoptosis of B7+ cells. The invention is cancer where B calls promote the growth and/or metastasis of tumours, B cell lymphoma, B cell laptacent, lymphoma, a cancer where B calls promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymphoma, B cell lymphoma, a given in diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, chinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 7C10, a primatised antibody user). The invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; 97_1 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein sequence of primatised form of the heavy chain of 7C10 antibody.
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                  361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                          361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                     KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                      AAU11539 standard; Protein; 476
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used in the inventic interleukin-2 (IL-2)

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Score 2577; DB 23;
Pred. No. 1.2e-146;
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Chimeric Homo sapiens.
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N-PSDB; AAT62513.
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                                                                                       2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
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                         monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaque primatized 7C10 heavy chain DNA.
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                                                                   Claim 6; Fig 8B; 81pp; English.
                                                                                                                                                                                                                               and graft-versus-host disease.
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                                                                                                                                                                                                                                                             476 AA;
    N-PSDB; AAT62510.
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This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipones and inhibits binding of these antigens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell) antipones and inhibits particularly autofimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic ansemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. Onest diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule; immunosuppressants. Blocking B7/CDS interactions production of interleukin-2 (IL-2), T cell proliferation and thibits production of interleukin-2 (IL-2), T cell proliferation and
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Macaca fascicularis.
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March 29, 2003, 09:06:23 ; Search time 48.9575 Seconds (without alignments) 1295.559 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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		Description	Primatised anti-hu	Macaque primatized	Protein sequence o	Primatised anti-hu	Macaque primatized	Protein semience	Human immine syste	Human immine avere	Monoclonal antibod	Anti-rhesus D reco
SUMMERTES		OI.		AAW63761	AAU11539	AAW01822	AAW63765	AAU11646	AAB36206	AAY44721	AAR93553	AAR93166
		DB	18	19	23	18	19	23	22	21	17	17
	Query	Length	476	476	476	476	476	476	473	470	475	472
d	Query	Match	100.0	100.0	100.0	99.6	99.6	93.6	88.4	87.8	96.6	86.3
		Score	2577	2577	2577	2309	2309	2309	2277.5	2262	2230.5	2223
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1 AAB26884 3 AAR22757 8 AAW14927 8 AAW14925 2 AAG3640 8 AAW14926			1 AAB7473 2 AAB74212 2 AAB76952 7 AAW05829 8 AAW11639 1 AAU77289 9 AAM63763	
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ALIGNMENTS

AAW01818 standard; Protein; 476 AA

RESULT 1 AAW01818

Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma. Primatised anti-human B7.1 antigen antibody 7C10 heavy chain. 96WO-US10053. 95US-0487550. Chimeric Macaca cynomolgus; Chimeric Homo sapiens. 25-MAY-1997 (first entry) (IDEC-) IDEC PHARM CORP. WO9640878-A1. 06-JUN-1996; 07-JUN-1995; 19-DEC-1996

Anderson DR, Brams P, Hanna N, Shestowsky WS;

WPI; 1997-108638/10.

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                                PCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPSVKFNMYVDGVEVHNA 316
                                                                                   KTKRREEQYNSTYRVUSULTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 376
                80 YNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGW-VDVWGP 138
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                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE GY INVENTION: Anti-TgE Antibodies (as amended)
FILE REFERENCE: POT18P2CIDICUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
RIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-06-17
PRIOR FILING DATE: 1992-06-17
PRIOR FILING DATE: 1992-06-17
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 8
LENGTH 453
                                                                                                80.4%; Score 2073; DB 9;
83.9%; Pred. No. 1.7e-106;
tive 21; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/09925179; Publication No. US20030044858A1; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
FEATURE:
                                                                                               Query Match
Best Local Similarity 83.99
Matches 396; Conservative
            LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS
                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                  US-09-948-429B-8
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US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Bresta, Leonard G Treating Allergic Disorders (as amended)
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; TITLE REFERENCE: PO718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 1992-03-15
; PRIOR APPLICATION NUMBER: US/08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR FILING DATE: 1994-01-26
; PRIOR FILING DATE: 1992-08-14
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US/07/8495
; PRIOR APPLICATION NUMBER: US/07/8495
; PRIOR PILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US/07/8495
; PRIOR FILING DATE: 1992-08-14
; NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                               80 YNPSLKSRVTISKDTSKNQFPLNLNSVTDADTAVYYCARGPRPDCTTICYGGW-VDVWGP 138
                                                                                                                                                                                                                                                                                             60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-----YFGHWHFAVWGQ 113
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                                                                              Length 453;
                                                                    80.3%; Score 2069; DB 9; Length 45
85.7%; Pred. No. 2.6e-106;
Live 19; Mismatches 37; Indels
OTHER INFORMATION: humanized maell, version 1 heavy chain
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85.7%; Pred. No. 2.6e-106;
iive 19; Mismatches 37;
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                                                                                                                    Matches 394; Conservative
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                                                                                             Best Local Similarity
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Best Local Simil
Matches 394; (
       ; UTHER INTO
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                                                                         Query Match
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us-09-758-173-4.rapb

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8 LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEW
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ZIP: 22314
ZIP: 22314
MEDIUWER READABLE FORM:
MEDIUWER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 70
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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                            WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 246
                                                                                                       KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 306
                                                                                                                           246 KSCDKTHTCPPCPAPELLGGPSVFLFPFKPKDTLMISRTPEVTCVVUDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                     KAKGOPREPOVYTL PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%; Score 2073; DB 9;
83.9%; Pred. No. 1.7e-106;
iive 21; Mismatches 51;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10124905
Patent No. US20020166136A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
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TELEFAX: 703-636-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 06
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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Matches 396; Conservative
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Sequence 8, Application US/09948429B
Sequence 8, Application US/09948429B
Sequence 8, Application General R.
PAPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREEL: 699 Prince Street
CITY: Alexandria
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126 -TICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
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                                                                                                                                                                                                                           VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA
                                                                                                                                                                                                                                                187 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA
                                                                                                                                                                                                                                                                                                           EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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Sequence 25, Application US/09740002

Sequence 25, Application US/09740002

GENERAL INFORMATION:
APPLICANT: MORROW PHILLIP
ITILE OF INVENTION: SPECIFIC TO RSV F-PROILITY HUMAN MONOCLONAL ANTIBODIES
ITILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
ITILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
CURRENT APPLICATION NUMBER: US/09/740,002

CURRENT FILING DATE: 1999-06-12-20
PRIOR FILING DATE: 1999-06-135,697
PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATCHIN UNIVERSITY OF SEC 
                                                                                                           80 YNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGW-VDVWGP 138
                                                                                                                                                                                                                                                       114 GTLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPBPVTVSWNSGALTSGVHT 173
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                                                                                                                                           60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSH-----YFGHWHFAVWGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
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                                     174 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
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     20 QVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGNGATTN
                                                                                                                                                                                                                       GDLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
                                                                                                                                                                                                                                                                                                                                      199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC
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84.9%; Pred. No. 1.2e-106;
live 25; Mismatches 43;
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Matches 399; Conservative
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                                                                           ; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table US-09-925-179-68
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                                                                                                                                                                                                                                                                                                                                                                                     80 YNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGW-VDVWGP 138
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| Patent No. US20020054814
| GENERAL INFORMATION:
| APPLICANT: Lowman, Henry B.
| APPLICANT: Lowman, Henry B.
| APPLICANT: Lowe, John
| APPLICANT: Lowe, John
| APPLICANT: Lowe, John
| TILLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
| FILE REFERENCE: P11.23_CUS
| CURRENT APPLICATION NUMBER: US/09/920,171
| CURRENT APPLICATION NUMBER: US 08/887,352
| PRIOR PILING DATE: 1997-07-02
| PRIOR FILING DATE: 1997-07-02
| PRIOR FILING DATE: 1999-04-21
| NUMBER OF SEQ ID NOS: 44
| SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                   Length 451;
                                                                                                                                                             Query Match 81.5%; Score 2099; DB 9; Length 4 Best Local Similarity 86.7%; Pred. No. 6e-108; Matches 397; Conservative 18; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18
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81.2%; Score 2092; DB 10;
Best Local Similarity 86.2%; Pred. No. 1.4e-107;
Matches 395; Conservative 19; Mismatches 36;
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TYPE: PRT ORGANISM: Artificial sequence
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US-09-920-171-18
                                                       FEATURE:
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PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
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APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 1097-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Heavy chain sequence derived from MAE11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.5%; Score 2100; DB 10;
86.5%; Pred. No. 5.3e-108;
iive 20; Mismatches 34;
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Patent No. US20020050548A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 396; Conservative
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US-09-920-171-16
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173
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                              20 QVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGNGATTN 79
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                                                          ; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16
                                                                                                                                                      Query Match 81.5%; Score 2100; DB 10; Length Best Local Similarity 86.5%; Pred. No. 5.3e-108; Matches 396; Conservative 20; Mismatches 34; Indels
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Sequence 66, Application US/09925179

Publication No. US20030044858A1

GENERAL INPORMATION:
APPLICANT: Jaracieu, Paula M.
APPLICANT: Jaracieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
FILE REFERENCE: PO718DP2C101C1US
CURRENT APPLICATION NUMBER: US/09/925,179

CURRENT APPLICATION NUMBER: US 08/466,163

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1991-08-14

PRIOR FILING DATE: 1991-08-14

PRIOR FILING DATE: 1991-08-14

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 68

LENGTH: 451
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TYPE: PRT ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Table US-09-925-179-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

81.5%; Score 2100; DB 9; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels
                                                                      APPLICANT: Presta, Leanard G.
APPLICANT: Presta, Leanard G.
TTTLE OF INVENTION: Atti-1gE Antibodies (as amended)
FILE REFERENCE: P0718P2C1DIGLUS
CURRENT APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-16
PRIOR FILING DATE: 1995-03-16
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1990-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1990-05-07
PRIOR FILING DATE: 1990-05-07
PRIOR FILING DATE: 1990-05-07
PRIOR FILING DATE: 1990-05-07
PRIOR FILING DATE: 1991-08-14
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Sequence 65, Application US/09925179
Publication No. US20030044858A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
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US-09-920-171-14
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US-09-925-179-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ب</u>
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81.6%; Score 2103; DB 9; Length 45
Best Local Similarity 86.7%; Pred. No. 3.6e-108;
Matches 397; Conservative 19; Mismatches 34; Indels
                                                                                                                                                               APPLICANT: Dardieu, Paula M.
APPLICANT: Dardieu, Paula M.
APPLICANT: Dresta, Leonard G.
TITLE OF INVENTION: Anti-19g Antibodies (as amended);
FILE REPERENCE: P0718P2C1D1C1US
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-06-06
PRIOR PILING DATE: 1995-03-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1992-03-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR PILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-08-07
PRIOR PILING DATE: 1992-08-07
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 66
LENGTH: 451
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                                                                                                    Sequence 66, Application US/09925179
Publication No. US20030044858A1
GENERAL INFORMATION:
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                                                  RESULT 5
US-09-925-179-66
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                                                                                                                                    COUNTRY: US
ZIP: 22314
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WONKEY WONCOLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFLLLUVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 89.6%; Score 2309; DB 9; Length 4
Best Local Similarity 91.2%; Pred. No. 2.1e-119;
Matches 434; Conservative 9; Mismatches 33; Indels
                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                           FILING DATE: 07-UW-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-836-6620
                                                                                                                                                                                               APPLICATION NUMBER: US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09948429B Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCI TITLE OF INVENTION: TO HUMAN B7.1
TITLE OF INVENTION: PHARMACEUTIAL
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 aning acids
                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-62021
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TYPCLIGY: linear
MOLECULE TYPE: protein
US-10-124-905-12
                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-948-429B-12
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61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TSM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
89.6%; Score 2309; DB 9;
Best Local Similarity 91.2%; Pred. No. 2.1e-119;
Matches 434; Conservative 9; Mismatches 33;
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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GY: linear
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Gaps

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Sequence 12, Application US/10124905
Patent No. US20020166136A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BUNNS, DOANE, SWECKER & MATHIS
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 2577; DB 9; Length Best Local Similarity 100.0%; Pred. No. 4.6e-134; Matches 476; Conservative 0; Mismatches 0; Indels
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-LABORESS:

-LABORESS:

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: 1107
                                                                                                 012712-131
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01273
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6201
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH 476 amino acids
TYPE: Allegar
                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-948-4298-4
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MEDIUM TYPE: Floppy
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US-10-124-905-12
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TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                 181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 EPVTVSWNSGALTSCVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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                                                                                                                                                                                                          1 MKHLWFFLLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                                                                                                                                                                                                                       1 MKHLWFFLLLVAAARWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                    Length 476;
                                                                                                                  100.0%; Score 2577; DB 9; Length (100.0%; Pred. No. 4.6e-134; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING BATE:
CLASSIFFCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
                                                                                                                                                              Matches 476, Conservative
                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-10-124-905-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
         amino acid
                                                                                                                Query Match
Best Local Similarity
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(without alignments)
1531.829 Million cell updates/sec
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1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476
                                                                                                                                    March 29, 2003, 09:14:52 ; Search time 18.2478 Seconds
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       237916 segs, 58723674 residues
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                            US-09-758-173-4
                                                                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                    Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1. /cgnz 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2. /cgnz 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3. /cgnz 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
4. /cgnz 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
5. /cgnz 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
6. /cgnz 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
7. /cgnz 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
8. /cgnz 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
9. /cgnz 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*
10. /cgnz 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
11. /cgnz 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
12. /cgnz 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
13. /cgnz 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
13. /cgnz 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
13. /cgnz 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*
14. /cgnz 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:* Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 4, Appli	12,	Sequence 12, Appl	Sequence 66, Appl	Sequence 65, Appl	ঝ	Sequence 16, Appl	~	Sequence 18, Appl	Sequence 25, Appl		Sequence 8, Appli	Sequence 8, Appli	Seguence 8, Appli	Sequence 8, Appli		Sequence 27, Appl	Sequence 230, App
SUMMARIES	αı	US-10-124-905-4	US-09-948-429B-4	US-10-124-905-12	US-09-948-429B-12	US-09-925-179-66	US-09-925-179-65	US-09-920-171-14	US-09-920-171-16	US-09-925-179-68	US-09-920-171-18	US-09-740-002-25	US-10-124-905-8	US-09-948-429B-8	US-09-925-179-8	US-09-802-077-8	US-09-802-096-8	US-09-726-258-71	US-09-740-002-27	US-09-996-288-230
	DB	6	σ	σ	6	თ	σ	10	10	σ	10	10	σ	σ	σ	10	10	6	70	თ
	* Query Match Length DB	476	476	476	476	451	451	451	451	451	451	475	478	478	453	453	453	452	475	451
	* Query Match	100.0	100.0	89.6	89.6	81.6	81.5	81.5	81.5	81.5	81.2	80.5	80.4	80.4	80.3	80.3	80.3	80.0	79.5	79.4
	Score	2577	2577	2309	2309	2103	2100	2100	2100	2099	2092	2075.5	2073	2073	2069	2069	2069	2061.5	2047.5	2047
	Result No.	1	7	m	4	2	9	٢	œ	6	10	11	12	13	14	12	16	17	18	19

App	App	App	Appl	Appl	App	App	App	Appl	Appl	Appl	Appl	Appl	Appl	App	Appl	Appl	App	App							
Sequence 216,	Sequence 218,	Sequence 250,	Sequence 43,	Sequence 49,	Sequence 220,	Sequence 222,		m	Sequence 39,	4	4	വ	N	Sequence 232,			Seguence 238,		Sequence 244,	Seguence 246,	Seguence 208,	Sequence 52,	Sequence 61,	Sequence 210,	Seguence 228,
US-09-996-288-216	US-09-996-288-218	US-09-996-288-250			US-09-996-288-220	US-09-996-288-222	US-09-996-288-224		US-09-796-848A-39			•	US-09-822-698A-26	US-09-996-288-232	US-09-996-288-234	US-09-996-288-236	US-09-996-288-238	US-09-996-288-242	US-09-996-288-244	US-09-996-288-246	US-09-996-288-208	US-09-825-012-52) US-09-825-012-61	US-09-996-288-210	US-09-996-288-228
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2045.5	2045.5	2045.5	2045.5	2045.5	2044.5	2044.5	2044.5	2044.5	2044.5	2044.5	2044.5	2044.5	2044	2042.5	2042.5	2042.5	2041.5	2041.5	2041.5	2041.5	2039.5	9	2039.5	2038.5	2038.5
20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B'1.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314

COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAREMENT Release #1.0, Version #1.30

CURRAIT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 31,030
TELECHONE: 703-836-620
TELECHONE: 703-836-620
                   ; Sequence 4, Application US/10124905; Patent No. US20020166136A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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STATE: VA
COUNTRY: USA
TO: 22314
US-10-124-905-4
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Sequence 16, Application US/09296005

Sequence 16, Application US/09296005

Patent No. 6390957

GENERAL INFORMATION:

APPLICATY: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides

FILE REPERENCE: P1123CIT

CURRENT APPLICATION NUMBER: US/09/296,005

CURRENT FILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-04-21

SEALIER FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 26

CONGANISM: Artificial

COCATION: 1-451

COCATION: 1-451

COCATION: 1-451

COCATION: 1-451

COCHER INFORMATION: Heavy chain sequence derived from MAEII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 YNPSLKSRVTISKDISKNQFFLNLNSVTDADIAVYYCARGPRPDCTTICYGGW-VDVWGP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVDFKSCDKTHTCPPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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414 LTVBKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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                                                             RESULT 15
US-09-296-005-16
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us-09-758-173-4.rai

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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides FILE REFERENCE: P1123GIr
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
BARLIER APPLICATION NUMBER: US 08/887,352
BARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
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  234 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 293
                                                                   319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
                                                                                          TLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
                                                                                                                                                                           354 TLPPSKEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRGLEWIGHIYGNGATTN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDG-STN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.5%; Score 2100; DB 4; Length 451; Best Local Similarity 86.5%; Pred. No. 1.5e-166; Matches 396; Conservative 20; Mismatches 34; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-296-005-14
                                                                                                                                                                                                                                       439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                               414 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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                                                                                                                                                                                                                                                                                                                                                                US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Artificial LOCATION: 1-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09109207C
Patent No. 6172213
GENERAL INPORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
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                       YNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGW-VDVWGP 138
                                                                                                                                                                  PPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDXKAEPKSCDKTHTCPPC 258
                                                                                                                                                                                                                                                                                 PAPELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
                                                                                                                                                                                                                                                                                                                                         KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
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                                                                                                                                                                                                                                                     PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
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LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
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CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
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US-09-109-207C-16
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US-09-109-207C-16
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LENGTH: 451 amino acids
              TYPE: Amino Acid
TOPOLOGY: Linear
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LENGTH: 451
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                    114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173
                                                                  199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
                                                                                      319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378
                                                                                                                                                                                                                        TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
                                                                                                                                                                                                                                                                                          Sequence 65, Application US/08466151
Fatent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                          439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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MEDIUM TYRE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: WINDBAIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
FILING DATE: 06-Jun-1995
FILING DATE: 15-MAR-1995
FILING DATE: 15-MAR-1995
FILING DATE: 15-MAR-1995
FILING DATE: 26-JAN-1994
FRIOR APPLICATION DATA: 26-JAN-1994
FRIOR APPLICATION DATA: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA: 1992
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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VSGUENCE 14, Application US/09109207C

Sequence 14, Application US/09109207C

Sequence 14, Application US/09109207C

Sequence 14, Application US/09109207C

Sequence 14, Application No. 617203

TYTILE NO. 617203

TYTILE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides

FILE REPERRICE: Improved Anti-1gE Antibodies and Method of Improving Polypeptides

FILE REPERRICE: 1998-06-30

CURRENT APPLICATION NUMBER: US 60/051,554

PRIOR PILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44
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Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps
                                                                                                                         8; Gaps
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                                                               Length 451;
                                                            Query Match
81.5%; Score 2100; DB 3; Length 4.
Best Local Similarity 86.5%; Pred. No. 1.5e-166;
Matches 396; Conservative 20; Mismatches 34; Indels
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; OTHER INFORMATION: Heavy chain sequence derived from MAE11
(MS-09-108-207C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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US-08-466-151-65
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Sequence 16, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                      294 KPREEQYNSTYRVVSVLIVLHQDWLNGKEYKCKVSNKALDAPIEKTISKAKGQPREPQVY 353
                                                                                                                                                                                                                                                                                                               379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
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                            199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC
                                                           174 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICHUHHHHHHHHHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                     319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
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                                                                                                                                                                                                                                                                                                                                                                                                               439 LTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                      414 LIVDKSRWQQGNVFSCSVMHEALHNYTQKSLSLSPGK 451
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NEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-701-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERNENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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STATE: California
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TYPE: Amino Acid
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US-08-887-352B-16
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Patent No. 594511
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                              241 DXKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                          301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                  292 EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351
                                                                                                                                                                                                                                     361 IEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNY 420
                                                                                                                                                                                                                                                              80 YNPSLKSRVIISKDISKNOFFLNLNSVIDADIAVYYCARGPRPDCTIICYGGW-VDVWGP 138
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175 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV 234
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                                                                                                                                                                                                                                                                                                                                                           412 KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNYTQKSLSLGK 467
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                                                                                                                                                                                                                                                                                                                               421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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86.5%; Pred. No. 1.5e-166;
tive 20; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinParin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
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ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTAIG G,
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112:
TELEPOMMUICATION INFORMATION:
TELEPOMMUICATION INFORMATION:
TELEPOMMUICATION INFORMATION:
TELEPOMMUICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 451 amino acids
TYPE: Amino Acid
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Matches 396; Conservative
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TOPOLOGY:
US-08-887-352B-14
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320 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 379
                                                                                                                                                                                 440 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                       410 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 446
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPRENCE/DOCKET NUMBER: 0127;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-523-894-10
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110 PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 229
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                                                          US-08-397-411-7; Sequence 7, Application US/08397411; Sequence 7, Application US/08397411; Patent No. 6129914; GENERAL INFORMATION:
APPLICANT: Gaingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: Begen 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
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81.7%; Score 2106.5; DB 3; Length 446;
Best Local Similarity 88.2%; Pred. No. 4.1e-167;
Matches 403; Conservative 16; Mismatches 27; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 01-MAR-1995
CLASSIFICATION WIDER: US/08/397,411
FILING DATE: 27-MAR-1995
ATTORNEY/ARDIT INFORMATION:
NAPL: Smith, William M.
REDISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INPORMATION:
TELECHOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
    APPLICANT: Hanna, Nabil
    APPLICANT: Reman, Roland A.
    APPLICANT: Reff, Mitchell E.
    TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
    TITLE OF INVENTION: Therapy
    NUMBER OF SEQUENCES: 59
    CORRESPONDENCE ADDRESS:
    ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
    CITY: ALEXANDARIA ADDRESS:
    CONTY: ALEXANDARIA
290 PREEQYNSTYRUVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                  LPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKL
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81.7%; Score 2104.5; DB 4; Length
Best Local Similarity 84.2%; Pred. No. 6.5e-167;
Matches 401; Conservative 24; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ---SNILKYLHWLLYWGQGVLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 467;
                                                                                                            COMPUTER: USA

ZIP: 2314-3187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC.COMPATIBLE
OPERATING SYSTEM: PC.DOS/MS.DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATONNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
82.0%; Score 2112.5; DB 4;
Best Local Similarity 84.5%; Pred. No. 1.4e-167;
Matches 402; Conservative 24; Mismatches 41;
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSBEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acida
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 703-02
TELEPHONE: 703-836-2021
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                                                                                     STATE: VI
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Sequence 8, Application US/08523894 Patent No. 6136310

RESULT 6 US-08-523-894-8

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61 PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCA--- 117
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               APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newfi, Mitchand A.
APPLICANT: Reff, Mitchand A.
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TOWNESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 467;
                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDTUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BAPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: OF-SEE-1995
CLASSIFICATION NUMBER: US/08/523,894
ATTONREY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKT NUMBER: 35,030
TELEPHONE: 703-836-620
TELEPHONE: 703-836-620
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENDAMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.9%; Score 2111.5; DB 4
84.5%; Pred. No. 1.7e-167;
iive 24; Mismatches 41;
                                                                                                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 84.59
Matches 402; Conservative
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MOLECULE TYPE: protein
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GENERAL INFORMATION:
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Query Match
Best Local Similarity 90.0%;
Matches 422; Conservative
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MOLECULE TYPE: protein
US-08-793-450-8
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US-08-523-894-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 FPEPVIVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PPGKGLEWIGYIYYSGSTL-YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPEPVTVSWNSGALISGVHIFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPEN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 APIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 PRPDCTTICYGGW-VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKHLWFFLLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSI-SGYYYWTWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08793450; Patent No. 6312690; GENERAL INFORMATION: APPLICANT: EDELMAN, LENA APPLICANT: APPLICANT: KACZOREK, MICHEL APPLICANT: KACZOREK, MICHEL APPLICANT: KACZOREK, MICHEL APPLICANT: KACZOREK, MICHEL APPLICANT: TAPABIHI, HASSAN TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS DITLE OF INVENTION ANTI-RHESUS DITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.4%; Score 2277.5; DB 4; Length 90.8%; Pred. No. 2.7e-181; tive 16; Mismatches 21; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acide
STRANDEDNESS: single
TOPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.8 Matches 434; Conservative
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                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
; LIBRARY: PANCTUT01
; CLONE: 1513264
US-09-049-672A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 CYGGWYDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
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Patent No. 6136110
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2206; DB 4; Length 472;
Pred. No. 2.4e-175;
9; Mismatches 34; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OFFRANTING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acide
TYPE: amino acide
TYPE: amino acide
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61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKQVPSLKLNSWTAADTAVYYCVRDR 120
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                                                                                                                         61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                EPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNIKV 240
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          Gape
                                                                     1 MKHLWFFLLLVAAPRHVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                               MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                       181 BPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                                                   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Guedler, Karl J.
APPLICANT: Guedler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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        Indele
        33;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF-0497 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09049672A; Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
        434; Conservative
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Patent No. 6113898
GENERAL INFORMATION:
TO CONTRIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCES.
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                         RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                              PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                      61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                                                  DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                        EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
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Pred. No. 6.6e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGIGTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,030
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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91.2%;
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Best Local Similarity
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US-08-487-550-12
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

Run on:

March 29, 2003, 09:06:24 , Search time 16.9126 Seconds (without alignments) 828.100 Million cell updates/sec

Perfect score:

US-09-758-173-4 2577 1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1. /ogn2_6/prodata/1/iaa/5A_COMB.pep:*

2. /ogn2_6/prodata/1/iaa/6A_COMB.pep:*

3. /ogn2_6/prodata/1/iaa/6A_COMB.pep:*

4. /ogn2_6/prodata/1/iaa/6B_COMB.pep:*

5. /ogn2_6/prodata/1/iaa/PcTUS_COMB.pep:*

6. /ogn2_6/prodata/1/iaa/PcTUS_COMB.pep:*

6. /ogn2_6/prodata/1/iaa/PcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 4, Appli	12,	4,	œ	12	œ	•	10	14	16,	65,	14,	16,	14,	16,	18	18	Sequence 2, Appli	7	18	ω,	ω̈́	ω̈	71,	71,		
SOMETHES	ID	US-08-487-550-4	US-08-487-550-12	-09-049		08-523-894-	US-08-523-894-8	-80	US-08-523-894-10	US-08-887-352B-14	US-08-887-352B-16	US-08-466-151-65	US-09-109-207C-14	US-09-109-207C-16	US-09-296-005-14	US-09-296-005-16	US-08-887-352B-18	US-09-109-207C-18	US-09-282-505-2	US-09-054-255-2	US-09-296-005-18	US-08-487-550-8	US-08-466-151-8	US-08-466-163B-8	US-09-027-449-71	US-09-026-985-71	US-09-121-952A-71	
	DB	, m	m	4	4	4	4	m	4	N	~	ო	4	4	4	4	N	4	4	4	4	m	m	4	m	4	4	
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de	Query	100.0	89.6	88.4	85.6	82.0	81.9	81.7	81.7	81.5	81.5	81.5	81.5	81.5	81.5	81.5	81.2	81.2	81.2	81.2	81.2	80.4	80.3	80.3	80.0	80.0	80.0	
	Score	2577	2309	2277.5	2206	2112.5	2111.5	2106.5	2104.5	2100	2100	2100	2100	2100	2100	2100	2092	2092	2092	2092	2092	2073	2069	2069	2061.5	О	2061.5	•
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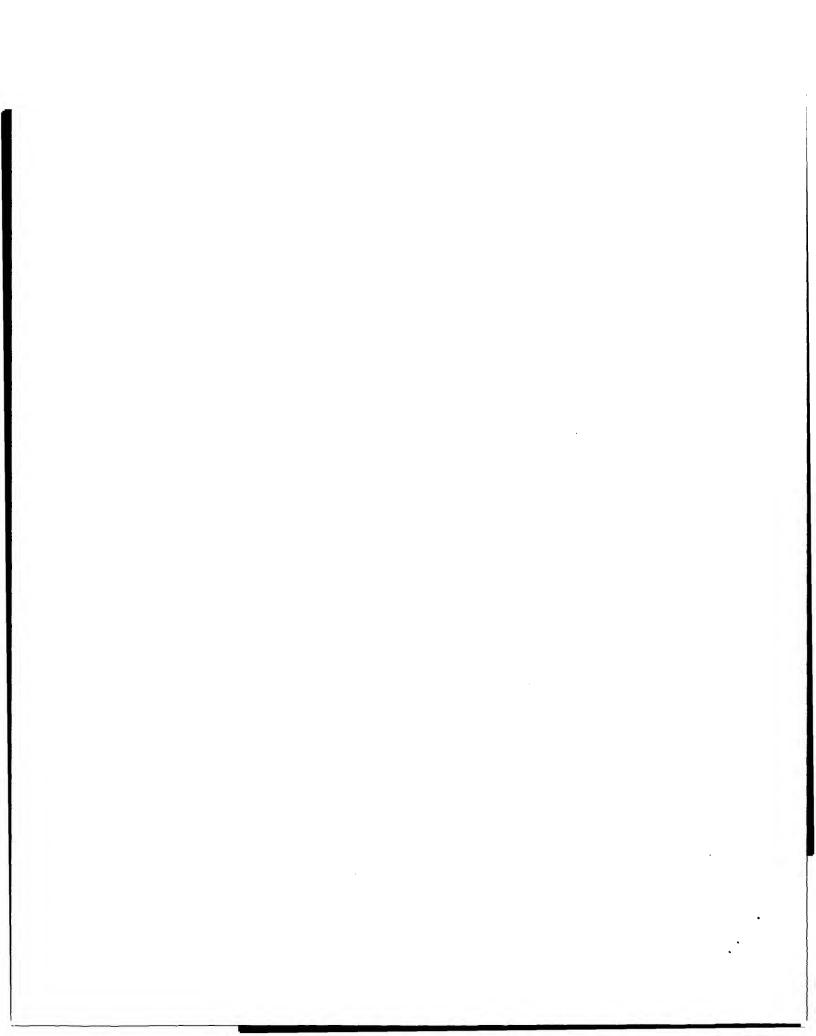
Sequence 10, Appl	Sequence 2, Appli	Sequence 13, Appl	Sequence 7, Appli	Sequence 30, Appl	Sequence 8, Appli		Sequence 18, Appl	_			_		Seguence 22, Appl	Seguence 3, Appli	Sequence 3, Appli	Seguence 9, Appli
US-08-378-939-10	US-09-6/9-39/-2 US-09-680-148-2	US-08-458-516-13	US-08-157-101A-7	US-09-301-593-30	US-09-049-672A-8	US-09-301-593-43	US-09-301-593-18	US-09-485-737B-67	US-09-485-737B-90	US-07-934-373C-22	US-08-437-642B-22	US-08-146-206C-22	PCT-US93-07832-22	US-09-247-352-3	US-09-466-635-3	PCT-US96-10043-9
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2039	2032.5	2025	2003.5	1998	1997.5	1978	1976.5	1961	1961	1960.5	1960.5	1960.5	1960.5	1949	1949	1886
28	9 6	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PARAMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFREENCE/DOCKET NUMBER: 35,030
REFREENCE/DOCKET NUMBER: 35,030
TELEPHONE: 703-886-6620
TELEPHONE: 703-886-6620
TELEPHONE: 703-886-2021
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
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100.0%; Score 2577; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-206;
Matches 476; Conservative 0; Mismatches 0;
                   Sequence 4, Application US/08487550 Patent No. 6113898 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-4
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US-08-487-550-4
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                                                                                          AB064102 BRI O2-JUL-2002 Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K6l.
AB064102 GI:21669410
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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genomics

AL Unpublished

CE 2 (bases 1 to 830)

JRS Kurosawa, I.

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyoake 470-1192, Japan

(E-mail:Kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL:http://www.fujita-hu.ac.jp/immunity/.

Location/Qualifiers

Location/Qualifiers

...... sapiens"
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone=lib="AIMS4"

/note="mixture of tissues:tonsils, umbilical cords,

peripheral blood and bone marrow"
                  718
661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGGGTT
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Pred. No. 1.3e-162;
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/gene="IGK"
/note="pelB signal peptide"
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/gene="IGK"
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Best Local Similarity 91.4%;
Matches 634; Conservative 0
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KEYWORDS
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145 CTTAAACACAGTAATGGAGACACCTTCCTGAGTTGGTATCAGCAGAAGCCAGGCCAACCT
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Primates; Catarrhini; Hominidae; Homo.
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                              61 GAAGTIGIGAIGACICAGICICCACIGICCCTICCCAICACACCIGGAGAGCCGGCCTCC 120
                                                    121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
                                                                                                                TATCAGCAGACCAGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
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Human monoclonal antibody against parathyroid hormone-related
Patent: JF 2000080100-A 4 21-MAR-2000;
JAPAN TOBACCO INC
ATGAGGNTCCNTGCTCAGCTCCTGGGGCTGCTAATGTTCTGGGTCTCTGGATCCAGTGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718
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JP 2000080100-A/4
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JP 2000080100-A/4.
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Mammalia; Eutheria;
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CI2R1:91)
(CI2N15/02, CI2R1:91), (CI2P21/08, CI2R1:91), CI2N5/00, CI2N15/00,
(CI2NS/00, CI2R1:91), (CI2N15/00, CI2R1:91)
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NOBUAKI HORI,CHIHIRO KUSUNOKI,MASASHI KAMATA
CO7K16/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TATCTGCAGAAGCCAGGGCAGTCTCTACAGCTCCTGATCTATTTGGGCTNTAATCGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC
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                                                                                                                                                                               Location/Qualifiers
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(1) . (60)
(61) . (60)
(398) . (717)
(230)
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_193 c 187 g
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/organism="Homo
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Best Local Similarity 89.4%;
Matches 642; Conservative
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540 540 600 900 99

480 480

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Homo saptene

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 720)

Hori,N., Kusunoki,C. and Kamata,M.

Human monoclonal antibody againet parathyroid hormone-related

DAPAN TOBACCO INC

OS Homo sapiens (human)

PN JP 2000080100-A/8

PD 21-MAR-2000

PP 12-OCT-1998 JP 1998304793

PR NOBUAKI HORI,CHIHIRO KUSUNOKI,MASASHI KAMATA

PC COTKI6/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,

PC COTKI6/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,

PC COTKI6/26,A61K31/00,A61K31/00,C12R1:91),C12N5/00,C12N15/00,

PC CC12N15/02,C12R1:91),(C12P21/08,C12R1:91),C12N5/10,

PC CC12N5/00,C12R1:91),(C12N15/00,C12R1:91)

PC CC12N5/00,C12R1:91),(C12N15/00,C12R1:91)

PC CC12N5/00,C12R1:91),(C12N15/00,C12R1:91)

PC CC12N5/00,C12R1:91),(C12N15/00,C12R1:91)

PC CTABE CONTRIBUTE

PC CTABE CONTRIBU
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C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                              601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAA 660
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                                                                                                                                                         421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
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                                                                                                                                                                                                                                                                                                                601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTNTACGCCTGCGAA
                                                          421 TICAICTICCCGCCAICTGAIGAGCAGTIGAAAICTGGAACTGCCICTGTTGTGTGCCTG
                                                                                                                        CTGAATAACTTCTATCCCAGAGGCCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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JP 2000080100-A/8.
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                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 720)
Hori, N., Kusunoki, C. and Kamata, M.
Human monoclonal antibody against parathyroid hormone-related
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COTKI6/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
A61K31/00,
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                                                                                                                                                                                                                                                                                                                   JAPAN TOBACCO INC
OS Homo sapiens (human)
PN JP 2000080100-A/7
PD 21-MAR-2000
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E35207.1 GI:18624435
JP 2000080100-A/7.
Homo sapiens.
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AUTHORS
TITLE
JOURNAL
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Human monoclonal antibody against parathyroid hormone-related
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                                                                                                                                                                                                Length 720;
                                                                                                                                                          others
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                                                                                                                                                                                                Score 599.4; DB 6;
Pred. No. 5e-163;
0; Mismatches 76;
. (397)
                                                                                                                                                          163
                                                                                                              (61).
(398).
(74)
                                                                                                    Location/Qualifiers
                                                        (349)
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                                           (80)
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Best Local Similarity 89.4%;
Matches 642; Conservative
    region
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Human monoclonal antibody against parathyroid hormone-related
protein.
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CO7K16/26, A61K31/00, A61K31/00, A61K31/00, A61K31/00,
A61K31/00,
A61K39/395, A61K39/395, C12N5/10, C12N15/02, C12P21/08//(C12N5/10,
C12R1:91)
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(CIZNIS/02,CIZRI:91), (CIZP21/08,CIZRI:91),CIZNS/00,CIZNIS/00,
(CIZNS/00,CIZRI:91), (CIZNIS/00,CIZRI:91)
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                  210
                                              264
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                                                                                                                                GCCAGTGGGTCAGGCACTGATTTCACACTGAAATCAGCAGGGTGGAGGCTGAGGATGTT 330
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                                                                       211 ccaagecectraatitataagetrictaaccegeacteresegreecagacagarreage 270
                                                                                                                                                            GGGCTTTATTTCTGCGGCAAGGTACAAGGACTCCTCCCACTTTCGGCGGAGGGACCAAG 384
 CTCGTACACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCT
                                                                                                    GGCAGTGGGGCAGGGACAGATTTCACACTGAAAATCAGCGCAGTGGAGGCTGAAGATGTT
                                                                                                                                                                                                                  GTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAG
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                                                                                                                                                                                                                                                                                                                                              GCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGTGTC
                                              Location/Qualifiers (1). (720) (1). (60)
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JP 2000080100-A/5
21-MAR-2000
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JP 2000080100-A/5.
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CDS
. sig_peptide
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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B30 bp mRNA linear PRI 02-JUL-2002 Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K65.
AB064106
AB064106.1 GI:21669418
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SRVBARDVGVYVGVYYMQGTHWPLIKGFTVEIKRTYAARSVFTPPSDGQLKSGTTASVV
CLLNNFYPRRAKVQNKUDNALQSGNSQESVTBQDSKDSTYSLGSTTJLSKADYBKHKY
YACEVTHQGLSSPVTKSFNRGECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGGGSG
                                                                                                                                                                                                                                                                                                     Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miraa,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKYLLPTAAAGLLLLAAQPAMADVVMTQSPLSLPVTLGQPASIS
                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 CTGTCCCTTCCCATCACACCTGGAGGCCGCCTCCATCTCCTGTAGGTCTAGTCAAAGC 144
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   663 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="K65"
/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 GGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGGGAAGTTGTGATGACTCAGTCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GGATTGTTATTACTCGCGCCCCGCCCATGCCCGATGTTGTGATGACTCAGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mali-kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="immunoglobulin kappa light chain VLJ /protein id="BAC01734.1" /db_xref="GI:21669419"
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                                                                                                                                                                                                             Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:K65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://www.fujita-hu.ac.jp/immunity/
Location/Qualifiers
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Yuqiu,J. and Mitcham,J.L.
Compositions and methods for the therapy and diagnosis of breast
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83.5%; Score 601.2; DB 6;
Best Local Similarity 89.8%; Pred. No. 1.5e-163;
Matches 645; Conservative 0; Mismatches 73;
                       DNA
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CORIXA CORPORATION (US)
             Sequence 51 from Patent WO0078960. AX067347.1 GI:12544971
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/db_xref="taxon:9606"
a 264 c 224 g 21.
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/product="Unknown (protein for MGC:22745)"
/protein id="AAH30814.1"
/db xref="C1:21410817"
/db xref="C1:21410817"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 607.6; DB 9;
Pred. No. 2.1e-165;
0; Mismatches 69;
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                                                                                                                note="Vector: pDNR-LIB"
                                         /tissue type="Prostate"
/clone lib="NIH MGC_83"
/lab host="DH10B"
  'db xref="taxon:9606"
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/codon_start=1
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al Similarity 90.4%;
649; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC010814 972 bp mRNA linear PRI 13-JUN-2
Homo sapiens, clone MGC:22745 IMAGE:4251290, mRNA, complete cds.
BC030814
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TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
                                                                                                                                                                                                                                                                                           TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
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                                                                         AGCGCAGTGGAGGCTGAAGATGTTGGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 972)
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RESULT 8 BC030814 LOCUS DEFINITION

ACCESSION

199 661

601 601 VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REMARK COMMENT

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540

RESULT 9

/organism="Homo sapiens"

source

FEATURES

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Gaps 9 90

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150 180 210 240

120

300 330 360 390 420 450 480 600

PAT 31-JAN-2002

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artificial sequences.
1 (bases 1 to 720)
Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S. Antihuman Fas humanized antibody-containing antirheumatic Patent: JP 2000154149-A 66 06-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A61K39/395, A61P29/00, C12N15/09//C07K16/28, C12P21/02, C12N15/00
     CTGAATAACTTCTATCCCAAGAGGCCAAAGTACAGTGGAAAGTGGAAAAGGCCCTCCAA 540
                                                                                  TCGGGTAACTCCCCAGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
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                                                               TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
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Antihuman Fas humanized antibody-containing antirheumatic.
E40695
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Pred. No. 3.4e-168;
0; Mismatches 63;
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/organism="synthetic construct"
/db_xref="taxon:32630"
a _200 c 184 g 156 t
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JP 2000154149-A/66
06-JUN-2000
17-SEP-1999 JP 1999263984
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Best Local Similarity 91.2%;
Matches 655; Conservative
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synthetic construct.
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PN JP 20
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NAKAHARA,
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                                                                                                                                                           artificial sequences.

Serizawa,N., Haruyama, H., Takahashi, W., Nakahara, K. and Yonehara, S. Serizawa, N., Haruyama, H., Takahashi, W., Nakahara, K. and Yonehara, S. Antihuman Fas humanized antibody-containing antirheumatic Sankyo Co LTD

Sankyo Co LTD

OS Artificial Sequence
PN JP 2000154149-A/68
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PR NOBUKI SERIZAWA, HIDEXUKI HARUYAWA, WATARU TAKAHASHI, PI KAORI NAKAHARA,
PR SHIN YONEHARA
PI CC Location/Qualifiers
FI Mat_peptide (61) . . (717)
FT mat_peptide (61) . . (717)
FT sig_peptide (61) . . (717)
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                                          E40697 720 bp DNA linear PAT 3:
Antihuman Fas humanized antibody-containing antirheumatic
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Pred. No. 1.2e-168;
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(1)..(717)
peptide (61)..(717)
peptide (1)..(61).
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
a _200 c 185 g 156 t
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Best Local Similarity 91.4%;
Matches 656; Conservative
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synthetic construct
                                                                                                                 JP 2000154149-A/68.
RESULT 6
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Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S. Antihuman Fas humanized antibody-containing antirheumatic Patent: JP 2000154149-A 67 06-JUN-2000;
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                                      Query Match 86.2%; Score 620.4; DB 6; Length 891; Best Local Similarity 91.5%; Pred. No. 4e-169; Matches 657; Conservative 0; Mismatches 61; Indels 0
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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FT ma_peptide (1)..(60).
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361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420
                     391 TCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC 450
                                                                     ITCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480
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AUTHORS
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JOURNAL
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// codon start=1
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/brotein id="AAH22362.1"
/brotein id="Id=18490211"
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STQSLVYSDGNTYLNWFQQRFGQSPRRLIYKVSNRDSGVPDRFSGGGSGTDFTLKITR
VEAEDVGVYFCMQGTHWPSTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL
LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 37 Row: b Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                             Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                 Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTIGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120
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/clone="MGC:2388 IMAGE:4704496"
/tissue_type="Lung"
/clone_lib="NIH MGC_77"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.3%; Score 628.4; DB 9;
ilarity 92.2%; Pred. No. 1.9e-171;
Conservative 0; Mismatches 56,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
Strausberg, R.
Direct Submission
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                                                                                                                                                           Ouery Match
100.0%; Score 720; DB 6; L
Best Local Similarity 100.0%; Pred. No. 4.5e-198;
Matches 720; Conservative 0; Mismatches 0;
Location/Qualifiers
1. .720
                                                    organism="unknown"
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REFERENCE

AUTHORS TITLE

ORGANISM

BC022362 LOCUS RESULT 2

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April 5, 2003, 19:13:05 ; Search time 2259.24 Seconds (without alignments) 9274.790 Million cell updates/sec
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720
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	864 Seque	ECOZZSOZ BOWO BADI E40698 Antihuman F	E40748 Antihuman F	E40696 Antihuman F	E4069/ Ancinuman F E40695 Antihuman F	BC030814 Homo sapi	AX067347 Seguence	ABU64106 HOMO BAD1 E35205 Human monoc	E35207 Human monoc	E35208 Human monoc	AB064102 Homo sapi	E35201 Human monoc	E35206 Human monoc	E35202 Human monoc	BC034142 Homo sapi	AK096938 Homo sapı	E35210 Human monoc	AB064059 Homo sapi	ABO64137 HOMO BADI AR064133 Homo Badi	AB064101 Homo sapi	AB064090 Homo sapi	AB064057 Homo sapi	AB064135 Homo sapi	AB064105 Homo sapi	ABO64104 Homo sapi	E10698 cDNA encodi	AB064055 Homo sapi	ABU64U58 Homo Bapi	112 HOM	191 Hom	MOH E60	153 Seg	AX076855 Sequence	240			linear PAT 14-FEB-2001					owsky, W.S. and Heard, C.	
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SUMMARIES	Ω	AR108864	BC022362	E40748	E40696	E40697	BC030814	AX067347	AB064106	E35207	E35208	E35204	E35201	E35206	E35203	BC034142	AK096938	E35210	AB064059	AB064137	AB064101	AB064090	AB064057	AB064136 AB064135	AB064105	AB064104	AB064054 E10698	AB064055	AB064058	AB064112 AB064092	AB064091	AB064093	AB064089	AX076855	AX277240	ALIGNMENTS		0	as	5140			ᅀᅜ	ibodies A S 05-SEP-2000
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TTCATCTTCCCGCCATCTGAGGAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCCTG 480
                                                                                                   CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540
                                                                                                                                301 AGCGCAGTGGAGGCTGAAGATGTTGGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
                      241 TCCGGGGTCCCTGACAGGTTCAGTGGAGTGGATCAGGCACAGATTTTACACTGAAAATC 300
                                                                                                                                                             AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 660
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Search completed: April 5, 2003, 20:19:19 Job time : 198.594 secs

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                                              New polynucleotides encoding breast tumor specific proteins, useful for prevention, treatment and diagnosis of breast cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGGTCCAGTGGG 62
                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                       1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the coding sequences for a number of breast cancer related proteins. These can be used in vaccinations against, diagnosis of and treatment of cancer, particularly breast
                                                                                                                                                                                                                                           61 GAAGTIGIGALGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC
                                                                                                                                                                                                                                                         63 GATATTGTGATGACTCAGTCTCCCAGCCCGTCACCCCTGGAGAGCCGGCCTCC
                                                                                                                                                                                                                                                                                  121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG
                                                                                                                                                                                                                                                                                               181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGGTAACTCCCAGGAGAGTGTCACAGAGGACAGCAAGGACAGCACCTACAGCCTC
                                                                                                                                                                  DB 22; Length 963;
                                                                                                                                                                                    73; Indels
                                                                                                                                            Sequence 963 BP; 253 A; 264 C; 224 G; 213 T; 9 other;
                                                                                                                                                               Query Match
83.5%; Score 601.2; DB 22;
Best Local Similarity 99.8%; Pred. No. 1.5e-150;
Matches 645; Conservative 0; Mismatches 73;
                                                                          Claim 25; Page 135-136; 165pp; English.
        Yuqiu J, Mitcham JL;
                           WPI; 2001-041426/05.
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The present invention describes a human monoclonal antibody to parachycrid hormone related protein (FTHTP). The monoclonal antibody or parachycrid hormone related protein (FTHTP). The monoclonal antibody or tits fragments, following the stimulation of FTHTP has the following properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits the release of calcium from bone; or (c) inhibits alevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumarcid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingira actual systemic inflammatory response syndrome (SIRS) and hypophosphateemia. It has antiarthritic, cytostatic and antianilammatory activities. The present sequence represents a human PTHTP monoclonal antibody clone nucleotide sequence from the
                                                                                                                                                                                                             Human, parathyzoid hormone related protein, FTHrP, monoclonal antibody, hypercalcaemia, rheumatoid arthritis, bone cancer; metaetasis, pain, fracture, cachexia, toth disease, periodontal disease, gingiva, espsis, systemic inflammatory response syndrome; SIRS, hypophosphataemia, antiarthritic, cytostatic, antinflammatory, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A human monoclonal antibody to parathyroid hormone related protein. - useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone including metastasis, and pain
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                                                                                                                                             Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.
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83.2%; Score 599.4; DB 21; Length 720;
Best Local Similarity 89.4%; Pred. No. 4e-150;
Matches 642; Conservative 0; Mismatches 76; Indels 0;
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98JP-0196729.
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                                                                    02-AUG-2000 (first entry)
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AAA13924;
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AAA13924 standard; DNA; 720 BP.

RESULT 15

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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to trast autoimmune diseases, especially consists. Included in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM molecule (see AAB12913-B12918 and ABB12919), and corresponding protein sequences (see AAB12913-B12918 and ABB12919), and cucleotide sequences of the humanised anti-human Fas Ig CH11 (see CaAA78202-A78266) and protein sequences (see AAB12913-08208-B12910). Also included are anti-human Fas antibody CDR peptides (AAA18202-B12910). Also chains used in the invention are represented by sequences AAA78210-B12910 and humanised anti-human Iga antibody and protein are represented by sequences AAA78213-A78266. Frincer used for sequences Dy Sequences AAA78213-A78266. Primers used for sequences AAA78213-A78266. Primers used for sequences AAA78213-A78318 and AAA78313-A78317, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78313-A78367. Primer used in the invention are represented by sequences AAA78313-A78367. Primer represented by sequences AAA78313-A78367. Primer conduction of the agent of the invention.
                                                                                           601 AGCAGCACCTGAGCGAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAA 660
601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAGTCTACGCCTGCGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #77.
                                                                                                                                                        661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTT 718
                                                                                                                                                                                 661 GTCACCCATCAGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTT 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism; anti-Fas antibody; ss.
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                                                                                                                                                                                                                                                                                                            AAA78267 standard; DNA; 720 BP.
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Best Local Similarity 91.21
Matches 655; Conservative
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P-PSDB; AAB12913.
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                                                                                                                              TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
                                                                                                                                                                              TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer related protein coding sequence SEQ ID NO: 51.
1 ATGAGGCTCCCTGCTCGAGGCTCCTGGGGCTGCTAATGCTCTGGGTCCCAGGATCCAGTGGG
                                                                                                                                                                                                                                                                                           CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAAGTGGATAACGCCCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAAGTTGTGATGACTCAGTCTCCAACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC
                                                GATGTTGTGTTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCC
                                                                                 121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGGTAATGGAGACACCTTCCTGAGTTGG
                                                                                                AGCGCAGTGGAGGCTGAAGATGTTGGGGGTTTTTTTTCTGCGGGCAAGGTACAAGGACTCCT
                                                                                                                                                                                                                                                                          CCCACTITCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC
                                                                                                                                                                                                                                                                                                                          TTCATCTTCCCCCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
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autoimmune disease; rheumatoid arthritis; therapy; human;
                      121 ATCTCCTGCAGATCTAGTAAGAGCCTTGTACACAGTAATGGAAACACCTATTTACATTGG
                                                                        TATCAGCAGAAGCCAACCTCCAAGGCTCCTGATTATAAGGTTTCTAACCGGGAC
                                                                                              TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGCAGGGACAGATTTCACACTGAAAATC
                                                                                                                                                                         TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATC
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This cDNA sequence codes for a humanised anti-Fas antibody CH11 light chain (see AAW71876), designated VL-KY. VL-KY is based on the light chain (see AAW71876), designated VL-KY. VL-KY is based on the light chain (see AAW71899) of murine anti-human Fas monoclonal antibody CH11. The humanised sequence was designed following selection of donor residues from CH11 to be grafted onto acceptor on molecule RPMIG410'CL. 4 Light chain sequences (see AAW71876-79) have been designed, and each can be used in combination with either of 2 humanised CH11 IgM antibodies that lack a J chain. These humanised cut-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as pHkappaKY2-58 including the VL-KY nucleotide (FERM BP-5861).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 617.2; DB 19; Length 720;
Pred. No. 7.2e-155;
0; Mismatches 63; Indels 0;
                                                                                                                                                                                                     Production of anti-Fas protein humanised antibodies - for us inducing apoptosis on Fas expressing cells in the treatment autoimmune diseases, especially rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 720 BP; 180 A; 200 C; 184 G; 156 T; 0 other;
Takahashi T;
   Serizawa N,
                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 92-93; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.2%;
Matches 655; Conservative
Nakahara K,
                                                                                                      WPI; 1998-482965/42
                                                                                                                                          P-PSDB; AAW71876
Haruyama H,
Yonehara S;
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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, sepecially rheumatism. The IgM molecule used in the invention has human Fasantigen binding properties. Included in the invention are nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AA78202-A78202-A7820) and heavy chains (see AA912913-B12918 and AAB12902-B12919), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AA78202-A78206) and protein sequences (see AAB12908-B12910). Also nucleotide are anti-human Fas antibody, Ilght, heavy and kappa chains used in the invention are represented by sequences AA78213-A7813 and AA78213-A78315. Primers used for sequences AA78217-A7818 and AA78213-A78315. Primer sequences AAA78213-A78318 and AAA78217-A78318 and AAA78217 9999999999999999999999988

Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;

ö 61 GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCC 120 121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180 181 TATCAGCAGAAGCCAAGCCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360 360 420 420 480 121 Arcreciacadareradadesecrieracadadadadadadesecrarradaride 180 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGCAGGACAGATTTCACACTGAAAATC 300 TTCATCTTCCCCCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540 CTGAATAACTICTATCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA 540 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGGACAGGACAGCTACAGCCTC 600 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCCCTACAGCCTC 600 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 660 AGCAGCACCCIGACGCIGAGCAGACCTACGAGAACACAAAAGICTACGCCIGCGAA 660 0; Gaps 9 1 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCCCAGGATCCAGTGGG 60 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 301 AGCAGGGTGGAGGTGTTGGGGGTTTATTTCTGCTCTCAAAGTACACATGTTCCT CCCACITITCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 361 CCGCCGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGTACTGTGGCTGCACCATCTGTC Trcarctrcccccarcrcarcaccacrrcaaarcrccaacrccrcrcrcrcrcrcrcrc Query Match
85.9%; Score 618.8; DB 21; Length 720;
Best Local Similarity 91.4%; Pred. No. 2.7e-155;
Matches 656; Conservative 0; Mismatches 62; Indels 0; 301 541 601 241 361 421 421 481 481 541 601 셤 ઠે 유 ò 임 ò g ò g ð g g ð ò 셤 g ઠે ò g ò 셤

The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypebtide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA78267-A78272) and the corresponding protein sequences (see AAA78267-A78272) and the nucleotide sequences of the humanised anti-human Fas antibody (DR peptides (AAB12912-B1299).

The Included are anti-human Fas antibody (DR peptides (AAB12902-B1290)).

Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAA78217-A78318 and AAA78335-A78337, while humanised anti-fas IgD DNA sequencing primers are represented by sequences AAA78318-A78337, while humanised anti-fas IgD DNA sequencing primers cepresented by sequences AAA78318-A78337. Primer represented by sequences AAA78338-A78337. Primer represented by sequences AAA78338-A783 61 GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCC 120 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120 0; Gaps 9 9 Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #81. Anti-human Fas humanizing antibody-containing antirheumatic agents 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 1 Arcadecrecerderecaderecrededecrecaderecredereceadarecadarede 61 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTT Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism; anti-Fas antibody; ss. Score 618.8; DB 21; Length 720; Pred. No. 2.7e-155; 0; Mismatches 62; Indels 0; Sequence 720 BP; 179 A; 200 C; 185 G; 156 T; 0 other; the production of the agent of the invention. Example 2; Page 69-70; 109pp; Japanese BP. Query Match
Best Local Similarity 91.4%;
Matches 656; Conservative 99JP-0263984. AAA78269 standard; DNA; 720 98JP-0264598. 16-NOV-2000 (first entry) (SANY) SANKYO CO LID WPI; 2000-454476/40. P-PSDB; AAB12915 JP2000154149-A. 18-SEP-1998; 17-SEP-1999; 06-JUN-2000 Synthetic AAA78269; RESULT 11 AAA78269 셤 ò g ò

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(FERM BP-5859).
                                                                             Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
autoimmune disease; rheumatoid arthritis; therapy; human;
antibody engineering; ds.
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                                                    Anti-human Fas humanised antibody CH11 light chain VL-RY cDNA
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Yonehara S;
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                                                                          181 TACCTGCAGAAGCCAGGCCAGTCTCCAAGGCTCCTGATCTACAAAGTTTCCAACCGATTT
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P-PSDB; AAB12914.
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autoimmune disease; rheumatoid arthritis; therapy; human;
antibody engineering; ds.
361 CCCACTTTCGGCGGAGGACCAAGGTGGAAATCAAAGGTACGGTGGCTGCACCATCTGTC
                                                    TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
                                                                                   CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
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P-PSDB; AAW71877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 618.8; DB 19;
Pred. No. 2.7e-155;
0; Mismatches 62;
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Best Local Similarity 91.4%;
Matches 656; Conservative
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41 Arcadecrecerecredecrecedescrectarians
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies comprising humanised light and heavy chains (see AAW71876-81) derived from the murine anti-human Fas monoclonal antibody CHII. The humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis.
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0
                                                                                                       Query Match 86.2%; Score 620.4; DB 19; Length 891; Best Local Similarity 91.5%; Pred. No. 1.1e-155; Matches 657; Conservative 0; Mismatches 61; Indels 0;
                                                                                  Sequence 891 BP; 204 A; 267 C; 225 G; 195 T; 0 other;
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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially chematism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody, Ight, heavy and kappa chairs maniful human Fas anti-human Fas anti-hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chains used in the invention are represented by sequences
AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the
invention are represented by sequences AAA78277-A78318 and
AAA78335-A78337, while humanised anti-fas Ig DNA sequencing primers are
represented by sequences AAA78321-A78334 and AAA78338-A78367, Primer
sequences AAA78212 are specific for murine Ig DNA, and are used in
the production of the agent of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-human Fas humanizing antibody-containing antirheumatic agents
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           autoimmune disease; treatment; rheumatism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 92; 109pp; Japanese.
                                                                                                                                                                                                                                              99JP-0263984
                                                                                                                                                                                                                                                                                                    98JP-0264598
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                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-454476/40.
     immunosuppression;
anti-Fas antibody;
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                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-human Fas Ig CH11 nucleotide SEQ ID #138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the invention are represented by sequences AAA78217-A78318 and AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78217-A78318 and AAA783218-A78335. AAA78212 are specific for murine Ig DNA, and are used in the production of the agent of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA/8267-A78272) and the nucleotide sequences (see AAA/8201-812918 and AAB1291), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AAA/8202-A78206) and protein sequences (see AAB12913-B12918). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
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                                                              Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human Fas humanizing antibody-containing antirheumatic agents
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                                                                                                    Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism; anti-Fas antibody; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 71-72; 109pp; Japanese.
                                                                                                                                                                                                                                                                                                                 99JP-0263984,
                                                                                                                                                                                                                                                                                                                                                         98JP-0264598
                      16-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of the DNA insert of plasmid pHL 15-27 encoding human immunoglobulin lighty chain (subgroup II). It was obtained from human lymphocyte CDNA by PCR amplification (see also AAV61367-68). The invention relates to novel humanised
                                                                                                                                                                                                                                                                      croantaactricrarcccagagaggccaaagracagragaaggragataacgcccrccaa
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                                               301 AGCGCAGTGGAGGCTGAAGATGTTGGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT
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Production of anti-Fas protein humanised antibodies - for use in
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Yonehara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV66632 standard; cDNA to mRNA; 891 BP
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                                                                                                                                                                                                                                                                       Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
autoimmune disease; rheumatoid arthritis; therapy; human;
                                                                                     TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACGACGACGACGACGACCAGCCTC
                                                                                              661 GTCACCCATCAGGGCCTGAGCTCGCCGGTCAAAGAGCTTCAACAGGGGGAGAGTGTTGA
CTGAATAACTTCTATCCCAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
                                                               GTCACCCATCAGGGCCTGAGCTCGCCCGTCAAAGAGCTTCAACAGGGGAGAGTGTTGA
                                       AGCAGCACCCTGACGCTGAGCAGAGCTACGAGAAACACACAAAGTCTACGCCTGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA sequence codes for a humanised anti-Fas antibody CH11 light Chain (see AAW71879), designated VL-RF. VL-RF is based on light Chain (see AAW71889) of murine anti-human Fas monoclonal antibody CH11, The humanised sequence was designed following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inducing apoptosis on Fas expressing cells in the treatment of autoimmune diseases, especially rheumatoid arthritis
                                                                                                                                                                                                                                                        Anti-human Fas humanised antibody CH11 VL-RF light chain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of anti-Fas protein humanised antibodies - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 100-101; 187pp; English.
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                                                                                                                                                                                                         AAV61362 standard; cDNA to mRNA; 720
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Yonehara S;
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selection of donor residues from CH11 to be grafted onto acceptor molecule RPMI6410'CL. 4 Light chain sequences (see AAW1876-79) have been designed, and each can be used in combination with either of 2 heavy chain sequences (see AAW1880-81) to provide novel, claimed humanised CH11 IgM antibodies that lack a J chain. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatchid arthitis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as pHkappaRF2-52 including the VL-RF nucleotide Requence, and host cells such as Escherichia coli pHkappaRF2-52 (FERM BP-5862).
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Pred. No. 3.8e-156;
0; Mismatches 60;
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Best Local Similarity 91.6%;
Matches 658; Conservative
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Anderson DR, Brams P, Hanna
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                                                                                    Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
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Matches 719, Conservative
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rejection of transplanted organ or tissue for treating proliferative and hyporproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the light chain of 786, a primatised antibody used in the invention to induce apoptosis.
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                                                                                                                      100.0%; Score 720; DB 24; Length 720; 100.0%; Pred. No. 2.7e-182; Live 0; Mismatches 0; Indels 0
                                                                                                Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;
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2 DNA sequences (AAT62511 and AAT13847) respectively code for primatised forms (AAW01819 and AAW01820) of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constent region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01817-18 and AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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Monoclonal antibody; cynomolgus monkey; macaque; 7B6; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lugus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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; Score 720; DB 19; Length 720; Pred. No. 2.7e-182; 0; Mismatches 0; Indels 0
    Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 720; Conservative 0
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7.4 cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allersy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or
                                                                                                                                                                                                                                                                                                                                                               Human, macaque monkey, light chain, primatised antibody, 7B6 antibody, neuroprotective, apoptosis inducer, allergy, CD28 receptor antagonist, B7 antigen, CD80, B7 antigen, CD80, B cell cancer, metastasis, tumour, B cell lymphomā, B cell leukaemia, autoimmune disease, jammunosuppression, organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
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               601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA
                                                                                                                         661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTGA
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/product= "Light chain of 786 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                       AAS17244 standard; DNA; 720
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Chimeric - Macaca sp.
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P-PSDB; AAU11540.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammallai, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Bases 1 to 738)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: Ggapba-r@mail.nih.gov
Tissue Proturement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at:
thtp://inage.linl.gov.a column: 04
High quality sequence stop: 845.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMIS42 row: column: 09
High quality sequence stop: 698.
                      431 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCCTG 490
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National Institutes of Health, Mammalian Gene Collection (MGC)
421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
                                                                                  CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
                                                                                                           491 CTGAATAACTTCTATCCCGGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
                                                                                                                                                                                              601 AGCAGCA-CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGA
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Contact: Robert Strausberg, Ph.D.
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/clone lib="NH MGC_113"
/lab host="DH10B (phage-resistant)"
/note="Corgan: spleen; Vector: porTs"; Site_1: XhoI; Site_2:
fnote="Corgan: spleen; Vector: porTs" Site_1: XhoI; Site_2:
ECORI; cDNA made by oilgo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
doCACGAG(6). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
superscript II RT (Life Technologies). Note: this is a
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602711509P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4851723 5',
mRNA sequence.
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                         /clone="IMAGE:6214761"
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S Nith-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Estrausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

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High quality sequence stop: 574.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                          TACCTGCAGAAGCCAGGCAGTCTCCACAGCTCCTGATCTTTTGGGTTCTCATCGGGCC 247
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                                                                                                                                                                                                                                                                   248 TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 307
                                                                                                                                                                                                                                                                                                                                  AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTTATTTCTGCGGGCAAGGTACAAGGACT-CC 359
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                                                                                                                                          181 TATCAGCAGAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC
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KEYWORDS
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:485355"
/clone="IMAGE:485355"
/clone="IMAGE:4853557"
/clone="IMAGE:4853557"
/tlab_host="DHIMG_YB =-cesistant)"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pDTB; Site 1: XhoI;
Site 2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp
following 5' adaptor: GGACGAG(G). Size-selected by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG758795 859 bp mRNA linear EST 15-MAY-2001
602713155F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853557 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
   CDNA Library Preparation: Ling Hong Rubin Laboratory
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLCM1669 row: m column: 14
   High quality sequence stop: 724.
   High quality sequence stop: 724.
   Location/Qualifiers
   rec
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                                                                                                                                                                                                                                                                                                                                                                                                  661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGGCTTCAACAGGGGAGAGTGTTGA 720
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1 (bases 1 to 859)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGATCCAGTGGG 67
       546 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
                                                                                                                                                                                                                                                           601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA
                                                                                                                                                                                                                                                                                                       606 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          666 GTCACCCATCAGGGGCTGAGCTCG-CCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGA
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                                                                                                                    541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
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Pred. No. 1.9e-157;
0; Mismatches 81;
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/clone="INMGGE-476453"|
/clone="INMGE-476453"|
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/clone="INMEG-48"|
/tissue type="primary B-cells from tonsils (cell line)"|
/tissue type="primary B-cells; vector: pOTB7;
/tote="Organ: B-cells; vector: pOTB7;
/note="Corgan: B-cells; vector: pOTB7;
/site_2: EcoR1; cDNA made by oligo-dT priming.
/birectionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8bb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI622 row: b column: 18
High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC 425
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1 (Dases 1 to 720)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 Nutional Institutes of Health, Mammalian Gene Collection (MGC)

3 Contact: Robert Strausberg, Ph.D.

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-romail.nih.gov/

7 Tissue Procurement: Life Technologies, Inc.

5 CDNA Library Preparation: Life Technologies, Inc.

6 CDNA Library Preparation: Life Technologies, Inc.

7 CDNA Library Preparation: Life Technologies, Inc.

8 CDNA Library Preparation: Life Technologies, Inc.

8 CDNA Library Preparation: Life Technologies, Inc.

8 CDNA Library Preparation: Life Technologies, Inc.

9 CDNA Library Preparation: Life Technologies, Inc.

1 CDNA Library Preparation: Life Technologies, Inc.

1 Location/Qualifiers
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/clone="INAGE:5207427"
/clone="lab".nlh MGC_122"
/lab host="bH108"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Slte=1: Not1; Slte=2: EcoRV (destroyed); RNA source anonymous do 20 4 24 week female lung, 16 week female spleen; and 20-22 week male spleens. Library is oligo-dT
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                                                                         GATAGETTCAGTGGCAGCGGGTCAGGGACAGATTTCACACTGAAAATCAGCCGGGTGGAG 301
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                                                 GACAGATTCAGCGGCAGTGGGGCAGGGACAGATTTCACACTGAAAATCAGCGCAGTGGAG
                                                                                                                                              GCTGAAGATGTTGGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCTCCCACTTTCGGC
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/organism="Homo sapiens"
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primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NHH MGC Library."
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                                                                                                                                                                                                                     DB 13; Length 720;
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                                                                                                                                                                                                                     Query Match 81.6%; Score 587.2; DB 13; Best Local Similarity 92.1%; Pred. No. 3.5e-160; Matches 641; Conservative 0; Mismatches 53;
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                                                                                                                                                                                                                             /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6277729"
/clone=lib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="OHN made by oligo-dT priming. Directionally cloned into EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
            Tissue Procurement: Dr. Mark Watson CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov.http://mage.llnl.gov.j column: 02 Plate: LLCMA464 row: j column: 02 High quality sequence stop: 645.
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Pred. No. 2e-161;
0; Mismatches 76; Indels 0;
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Email: cgapbs-r@mail.nih.gov
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/note="Organ: B-cells; Vector: pOTB7; Site 1: Xho1; Site 2: EcoR1; cDNA made by oligo-dT priming.

Directionally cloned into EcoR1/Kho1 sites using the following 5' adaptor: GGCACGAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH MCC Library."
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                                                                                                                                                                                                                                                                                                                                               BG758592 952 bp mRNA linear EST 15-MAY-2001
602712820F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853045 5',
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S NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-rémail.nih.gov.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CLONA Gistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL)

Http://image.llnl.gov

Plate: LicM1698 row: h column: 06
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="INAGE:4853045"
/clone="INAGE:4853045"
/clone="tib="NIH MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="primary B-cesistant"
/lab_host="phi08 (phage-resistant")"
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                                                                                                                                                  667 GICACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCNAACAGGG 716
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/organism="Homo sapiens"
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Location/Qualifiers
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BG758592.1 GI:14069245
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us-09-758-173-5.rst

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0; Mismatches
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      σ
    193
                                           82.3%;
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                                                            Best Local Similarity 90.8
Matches 654; Conservative
    200
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                                             Query Match
   BASE COUNT
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AUTHORS
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COMMENT
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BQ712430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM007723 726 bp mRNA linear EST 30-OCT-2001
603617168F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440961 5',
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

Lu fupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Profurement: Dr. Mark Watson

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 724.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 726)
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                                                                                     CACTITICGGCGGAGGACCAAGGIGGAAAICAAACGIACGGIGGCIGCACCAICIGIT
                                                                                                                                             CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT
                                                                                                                                                                 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCTGCT
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BM007723.1 GI:16522077
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KEYWORDS
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                              303
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AUTHORS
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JOURNAL
COMMENT
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BM007723
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AGENCOURT 8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
5', mRNA Sequence.
BQ712430.1 GI:21851329
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                    1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG
                                                                                                                                       8 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCCCAGGATCCAGTGGG
                                                                                                                                                                                                                               GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCTTGGACAGCCGGCCTCC
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     Length
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  DB 13;
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Score 592.4; DB 13
Pred. No. 1.1e-161;
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Matches 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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                                                                                                                                                                                                            1. 918
| /organisme"Homo sapiens" | 1. 918 | /organisme"Homo sapiens" | /db xref="taxon.9606" | /dlone=InAdez.4752888" | /clone=Inbe"INGIC GAP.8kn4" | /tissue_type="squamous cell carcinoma" | /lab.host="DHIOB (TI phage-resistant)" | /note="Organ: skin; Vector: pCWV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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           Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10611 row: k column: 01
High quality sequence stop: 866.
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Contact: Robert Strausberg, Ph.D.
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AGENCOURT_8495209 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301714 S', mNNA sequence.
BQ708918
BQ708918.1 GI:21847817
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2518 row: a column: 11
High quality sequence stop: 664.
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
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669 TCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTT
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/db xref="texon:9606"
/clone="IMAGE:6301714"
/clone lib="NIH MGC 113"
/lab_host="DH10B" (phage-resistant)"
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/note="Organ: pooled colon, kidney, stomach; Vector: pCWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: Lhis is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI758820 857 bp mRNA linear EST 25-SEP-2001 603042739F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183408 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1457 row: m column: 09
High quality sequence stop: 847.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                      GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 717
                                       368 ATCACCTICGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTC
                                                                                CCCACTITICGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC
                                                                                                                                                                   CTGAATAACTTCTATCCCAGAGGCCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5183408"
/clone lib="NIH MGC_116"
/lab_host="DH10B"
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BI758820.1 GI:15750398
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602627806F1 NCL_CGAP_SKn4 Homo sapiens cDNa clone IMAGE:4752888 5',
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                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                248 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATC 307
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                                                                                      8 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTCATGCTCTGGGTCCCAGGATCCAGTGGG
                                                                      ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG
                                                                                                                                                                                                                                                                          181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCAGGGACAGATTTCACACTGAAAATC
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21
     DB 13; Length
   Score 598.2; DB 13;
Pred. No. 2.4e-163;
0; Mismatches 53;
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BG681688
BG681688.1 GI:13913085
 83.1%;
                                     Conservative
                     Similarity
Query Match
Best Local Simi
Matches 665;
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BM007808
BM007808.1 GI:16522162
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Best Local Similarity 91.6%;
Matches 657; Conservative
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                                                    DEFINITION
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TITLE
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RESULT 2
BM007808
                                                                                           ACCESSION
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             /organism="Homo saplens"
/db.xef="taxon:9606"
/clone="IMAGE:5183446"
/clone lib="NIH MGE:5183446"
/lab host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pcMv-SPORT6; Site=1: Not!; Site=2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon, 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 489
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.9%; Score 618.8; DB 13; Length 816; Best Local Similarity 91.4%; Pred. No. 2.3e-169; Matches 656; Conservative 0; Mismatches 62; Indels 0;
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1. 774

| Organisms="Homo sapiens" | Aborte="Transcriptor" | Aborte="Lawn:9606" |
| Aborte="InAGE:5440662" |
| Clone=Tib="NIH MGC 113" |
| Alborte="Drive is provided by the p
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603617276F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440962 5',
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1914 row: h column: 19
High quality sequence stop: 770.
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Pred. No. 5.4e-167;
0; Mismatches 59; I
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BQ709417 BG755003 BG547597 BG740066

602714763 603061638

BI837183 BG75401 BG757588 BI518518 BI518518 BI508655

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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603069231 603083638

AGENCOURT

602243920 603032958 602575404

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BG530186 BI819546

602714967

BI838327 603083265 BG565315 602582819 BF238157 601811882

AGENCOURT

BQ711273 A BG757678 6 BM768355 K

BG758924 602713036 BM783161 K-EST0061 BQ711051 AGENCOURT BG745349 602723677 BQ709375 AGENCOURT

BI838136 BI908319 BF974515 AW404795

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
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I (Jaases I to 816)
INIH-MCC http://mgc.nci.nih.gov/.
INIH-MCC http://mgc.nci.nih.gov/.
Inititutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIL457 row: n column: 23
High quality sequence stop; 814.
Location/Qualifiers
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603043095F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5183446 5',
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AUTHORS
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BM007808 603617276
BI758820 603042739
BG681688 602627806
BQ708918 AGENCOURT
BM007723 603617168
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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FEATURES

Score

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DR InterPro; IPR003596; Ig_v.

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EXMART; SM00406; IGv. 1.

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Search completed: March 29, 2003, 09:11:14 Job time : 6.69846 secs

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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Marsh P., Mills F., Gould H., "Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE-89128968; PubMed-6441768;
ARDAINE-8128978. Herbar H., Grutter T., Chang J.Y., Braun D.G.;
"Muxine V kappa 25 and V kappa 27 amino-acid sequences of C5781/6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-IV REGION B17.
FRAMEWORK-1.
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                              Marsh P.; Submitted (OCT-1986) to the EMBL//GenBank/DDBJ databases.
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23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region 17829.1.
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                                                                        Nucleic Acids Res. 13:6531-6544 (1985)
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InterPro; IRW003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
PEam; PF00047; ig; 1.
SMART; SW00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X02990; CAA26733.1; -. PIR; A01905; K4HU17.
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| 121 PWTFGQGTKVEIKR 134
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                                                                                                                        REVISION TO 76.
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KVZE MOUSE
P03976;
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SEQUENCE
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MEDLINE=79012520; PubMed=99744;
MKSean D.J., Bell M., Potter M.,
MRchanisms of antibody diversity; multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQAVFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLLYQMSNLA 60
origin: monoclonal antibodies 17829.1 and 22825.1 specific for the group A-etreptococcal polyasccharide."; Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
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Biochemistry 17:2392-2400(1978).
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDILINE-7140252; Pubmed=4691517;
MEDILINE-71402525; Pubmed=4691517;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemiatry 12:760-771(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYCAHNLELPYTFGGGTKLEIKR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 404; DB 1; Length 113; 68.1%; Pred. No. 3.4e-26; Live 14; Mismatches 22; Indels
                                                                                                                                                                                                                         FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                           12390 MW; 4E93797046F8DB33 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region MOPC 63 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv. 1.
Immunoglobulin V region; Hybridoma.
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InterPro; IPR003006; Ig_MHC.
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39
54
102
112
113
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HSSP; P01607; IREI.
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KV3M HUMAN
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 YQOKPGQPPRLLIYGASTRATGIPARFSGSGSGTEFTLTISRLGSEDFAVYYCQQYNNWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSLPAQLIGLILICVPGSSGEVVMTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSW 60
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Goldfien R., Carson D.A.;
Goldfien R., Carson D.A.;
Ilight-Chain gene.",
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                       20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
19 kappa chain V-lil region CLL precursor (Rheumatoid factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-III REGION CLL. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%; Score 414; DB 1; Length 129; 60.4%; Pred. No. 6.3e-27; Live 23; Mismatches 24; Indels
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JK1 SEGMENT
                                                                    PRT;
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MEDLINE=86177570; Pubmed=3083417;
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InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406, IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M12740; AAA58992.1; -. PIR; A01898; K3HUCL.
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                                                                     STANDARD;
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116 PWTFGQGTRVEIKR 129
120 IPTFGGGTKVBIKR 133
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                                                                  KV3H HUMAN
P04207;
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DISULFID
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SEQUENCE
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Matches
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RESULT 12 KV3M_HUMAN

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61 YQQKPGQPPKLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
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MEDILINE=88171307; PubMed=3127527;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autcoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunorherapy.";

J. Exp. Med. 167:440-852 (1988).

-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUCOANTIC
                                                                                                                                              Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Score 414; DB 1;
61.7%; Pred. No. 6.3e-27;
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01-JAN-1988 (Rel. 06, Created)
01-AR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-IV region B17 precursor.
Homo sapiens (Human).
                                                                Last sequence update)
Last annotation update)
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  129 AA.
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                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update
15-JUL-1999 (Rel. 38, Last annotation upda
1g kappa chain V-III region HIC precursor.
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PRT;
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MEDLINE=86041854; PubMed=2997713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fmmunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P80362; IWTL.
INTERPO; IPR003006; Ig_MHC.
INTERPPO; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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STANDARD;
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                                                                                                                              Homo sapiens (Human).
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PIR, PLO021, KHUHI.
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129
129 AA;
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H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilechmann N.;
"Molecular basis of antibody formation.";
Maturalseenschaften 56:195-205(1969).
"IN MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
"IN MISCELLANBOUS: THE IS A BENCE-JONES PROTEIN.
HISTP, A01885, KZHUCM.
HISSP, P01607; IREI.
INTERPRO, 1PR0030596; Ig MHC.
InterPro, IPR0030596; Ig WHC.
Pfam; PP00047; ig; 1.
SMARKT; SMO0406; IG, 1.
DISULEDD 040; IS I.
DISULEDD 124 959; BEN SIMILARITY.
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Hilschmann N.;
"The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                      IG KAPPA CHAIN V-III REGION HAH.
FRAMEWORK-1.
                                                                                                                                           COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JAXI SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     34.0%; Score 422; DB 1; Length 129; 62.4%; Pred. No. 1.4e-27; ive 21; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                             14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-II region Cum.
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MEDLINE=70063440; PubMed=4188189;
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 62.4
nes 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PTFGGGTKVEIKR 133
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                                                                                                                                                                                                                                                                                                                                                 129 J
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82; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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P01614;
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Best Local S:
Matches 82
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                                                   61
21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHS-NGDTFLSWYQQKPGQPPRLLIYKVSNR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Subgroup IV of human immunoglobulin K light chains is encoded by a
                              2 DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSGDGNTYLNWYLQKAGQSPQLLIYTLSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                         ch 33.8%; Score 420; DB 1; Length 133; l Similarity 64.2%; Pred. No. 2.1e-27; 86; Conservative 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG KAPPA CHAIN V-IV REGION JI.
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                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-IV region JI precursor.
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                           PRT; 133 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; ig; 1.
Immunoglobulin V region; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                           STANDARD;
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133 1
133 AA;
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Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
Biochemistry 15:3829-383(1976)

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=88171307; PubMed=3127527;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autoantibody-associated kappa light chain variable region gene
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVVWTQSPLFLPVTLGEPASIQCRSSQSLVYRBGBTYLBWYLQKPGQSPELLIYLSSYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. EXD. Med. 167:840-852(1988).
-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
Ig kappa chain V-II region FR.
Howo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 FRAMEWORK-1.
39 CCMPLEMENTARITY-DETERMINING-
54 FRAMEWORK-2.
61 CCMPLEMENTARITY-DETERMINING-
93 FRAMEWORK-3.
102 CCMPLEMENTARITY-DETERMINING-
112 FRAMEWORK-4.
93 BY SIMILARITY.
93 BY SIMILARITY.
91 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.6%; Score 430; DB 1; 71.7%; Pred. No. 2.7e-28; iive 13; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Kappa chain V-III region HAH precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                             MEDLINE=76253627; PubMed=821524;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig MHC. InterPro; IPR003596; Ig_v. Pfan, PF00047; ig; I. SMART; SM00406; IGv; I. Immunoglobulin V region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                        PIR; A01886; K2HUFR.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
555
62
94
103
113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                 NCBI TaxID=9606;
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P18135;
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                                                                                                    Gaps
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"The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                   21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEABDVGVYYCMZALQAPITFGQGTRLEIKR 113
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                                                  Length 113;
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COMPLEMENTARITY-DETERMINING-3.
                                                                                                    15; Indels
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  12316 MW; 0C3C38F81F1843CA CRC64;
                                                  36.5%; Score 453; DB 1; 75.2%; Pred. No. 3.7e-30; iive 13; Mismatches 15;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; l.
SMART; SM00406; IGv; l.
Imminoglobulin V region; Bence-Jones protein.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region MIL.
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les 79; Conservative
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HSSP; P80362; 1WTL.
  113 AA;
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                                                                                                                                                                                                                                                                                                                                                           1 GSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Biochemistry 22:1153-1158 (1983).
-!- MISCELANEOUS: THIS CIRIN WAS ISOLATED FROM AN IGG2A HYBRIDOWA PROTEIN THAT BINDS DIGOXIN.
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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                                                                                                                                                                                     IG KAPPA CHAIN V-II REGION GM607.
FRAMEWORK-1.
                                                                                                                                                                                                                                                                                                         Score 487; DB 1; Length 117;
Pred. No. 7e-33;
8; Mismatches 15; Indels
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                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-3.
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HSSP; P80362; IWTL.
InterPro; IPR0031006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig, 1.
SWART; SM00406; IGv.
Immunoglobulin V region; Monoclonal antibody; Hybridoma.
                                                                                                                                                                                                                                                                                       12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region 26-10.
                                                                                                                                                                                                                                                                                                   39.2%; Scc. 80.3%; Pred. No. ,c. 81.3%; Pred. No. ,c. 81.3%; Pred. Nismatches
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                                                                                      EMBL; Z00009; -; NOT_ANNOTATED_CDS
                                                                                             | PIR; A01889; KZHUGM. | HSSP; P80362; IWTL. | INTERPRO; IPR003006; Ig_MHC. | INTERPRO; IPR003596; Ig_V. | Pfam; PF00047; ig; 1. | SMART; SM00406; IGV; 1. | SMART; SM00406; IGV; 1. | Immunoglobulin V region; Signal. | SIGNAL | A | IG KA | CHAIN | S | 17 | IG KA | DOMAIN | S | 17 | FRAME
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                                                                                                                                                                                                                                                                                                                   l Similarity 80.3
94; Conservative
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Glenner G.G.;
Structural identity of Bence Jones and amyloidosis.";
patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281(1973).
I. MISCELLANBOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISCHARD SEAME PATIENT.
II. MISCELLANBOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
IMISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a
                               COMPLEMENTARITY-DETERMINING-1.
                                                                                        COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                             Length 113;
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COMPLEMENTARITY-DETERMINING-1.
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HSSP; POLGO7; INEI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR00047; ig; 1.
Immunoglobulin V region; Bence-Jones protein; Amyloid.
                                                                                                                                                                                                                                                                              12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                          37.9%; Score 471; DB 1; 77.9%; Pred. No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region TEW.
                                                                                                                                                                                                                  BY SIMILARITY.
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FRAMEWORK-1
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.9%
Matches 88; Conservative
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Biol. Chem. 244:3550-3560(1969).

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           61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                        61 FQQRPGQSPRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120
                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN EU).
MEDLINE=71064023; PubMed=5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-69234734; PubMed=4893682; Tatani K., Shinded T., Putnam F.W.; Tani K., Shinded T., Putnam F.W.; "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete amino acid sequence of Bence Jones protein Cum (kappa-
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MEDLINE=81042304; PubMed=6775818;
Hieter P.A., Max B.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
"Cloned human and mouse kappa immunoglobulin constant and J region
genes conserve homology in functional segments.";
Cell 22:197-207(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN ROY).
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franek F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
                                                                                                                                                                                                                                                             Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gall W.E., Edelman G.M.;
The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds ";
Biochemistry 9:3188-3196(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 kappa chain C region.
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                                                                                                                                                        STANDARD;
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121 WTFGQGTKVEIKR 133
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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P01834;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                    Science 169:56-59(1970).
-!- MISCELAMBOUST THE BU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
--- MISCELAMBOUST THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
MARKER, 45-ALA AND 83-LEU.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                  MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FITG=VAR 003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

51984D1FDD372CE8 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region GM607 precursor (Fragment).
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SMAAT; SM00407; iGc!, 1.
PROSITE; PS00290; iG MF0.
Immunoglobulin domain; Immunoglobulin C region.
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57 57 E
106 AA; 11609 MW;
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Genew; HGNC:5716; IGKC.
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83
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Nature 309:73-76(1984).
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Query Match 44.3%; Score 550; DB 1; Length 133; Best Local Similarity 80.5%; Pred. No. 6.6e-38; Matches 107; Conservative 13; Mismatches 13; Indels
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Maximum DB seq length: 200000000
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NyAlternate names: immunoglobulin light chain
NyAlternate names: immunoglobulin light chain
Syspecies: Ms musculus (house mouse)
Cyspecies: Ms musculus (house mouse)
CyAccession: S68241; S68214
Synda, X.; Xhada, X.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrian A; Mseference number: S68241
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus
C;Species: Mus musculus
C;Species: Musculus
C;Accession: S37484
R;Ducancel, F.F.D.
Submitted to the BMBL Data Library, February 1993
A;Reference number: S37483
A;Reference number: S37483
A;Reference number: Musculus Mu
                                                                                                                                                                                                                                                                     80 DSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Accession: S68241
;Molecule type: mRNA
;Residues: 1-218 <TpK>
;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
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                                               Gaps
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                                                                                                                                                          21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGD-TFLSWYQQKPGQPPRLLIYKVSNR
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Local Similarity 61.4%; Pred. No. 2.1e-42; nes 135; Conservative 34; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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A; Residues: 1-225 < DUC>
   Best Loca
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R,Takagi, M.; Kohda, K.; Hamuro, T.; Haxada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FBBS Lett. 375, 273-276, 1995
A,Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin i A;Recession: S68211; MUID:96085223; PMID:7498516
A,Accession: S68214
A,Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                   Length 218;
                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 'NI',3-212 <TAM>
A;Crosez-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                             Query Match 55.9%; Score 694.5; DB 2; Best Local Similarity 59.4%; Pred. No. 1.9e-40; Matches 130; Conservative 35; Mismatches 53;
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ne : 11.7265 secs
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Ig kappa chain precursor - rat
CiSpecies: Rattus norvegicus (Norway rat)
CiDate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
CiAccession: 506084
RiCrowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nuclectide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
A;Reference number: 506084; MUID:90016888; PMID:2508067
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A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rosidues: 1-220 <SCH>
A;Rosidues: 1-220 <SCH>
A;Rosidues: 1-220 <SCH>
A;Coss-references: GB:M23626, GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
A;Coss-referamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
79 RDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Residues: 12-40 <CRO>
A.Cross-references: EMBL:X16129, NID:g56457, PIDN:CAA34256.1; PID:g56458
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin Schores: heterotetramer; immunoglobulin prodicted <SIG>
F:1-20/Domain: signal sequence #setatus predicted <SIG>
F:1-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>
                                    65 RFSGVPDRFSGSGSGSTBFSLEISRVEAEDLGVYYCFGSSHVRWTFGGGTKLEIKRADAAP
                                                                                                                                    139 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY
                                                                                                                                                                                QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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61.7%; Pred. No. 3.1e-45;
ilve 34; Mismatches 57;
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Best Local Similarity
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C;Species: Mus musculus (house mouse)
C;Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C;Accession: JL0029 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C;Accession: JL0029 #S.; Desaymard, C.; Scharff, M.D.
F;Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A;Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor A;Reference number: JL0029; MUID:88171315; PMID:3127529
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A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;14-93/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 VPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSVFI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 VMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRDSG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A.Residues: 1-225 cCH1>
A.Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A.Note: the authors translated the codon CGG for residue 106 as Pro,
A.Note: the nucleotide sequence shown is inconsistent with authors' the cacept for four positions shown above
c. Comment: The protein is an anti-phosphorylcholine antibody.
C.Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                              Ig kappa chain - mouse
C.Species: Mus musculus (house mouse)
C.Jate: 06-Jan-1995 #sequence_revision 06-Jan-1995
C.Accession: S42772
R.Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
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64.7%; Pred. No. 1.5e-45;
ive 32; Mismatches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-93/Domain: immunoglobulin homology <IMM>
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Matches 1443; Conservative 3
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Length 220;

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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Date: 21-Nov-1999 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S16112 M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; F B;O. Chem. Hoppe-Seyler 372, 451-453, 1991 A.Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(; A;Reference number: S16112; MUID:92000313; PMID:1910583 A;Accession: S16112 A;Accession: Inmunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 219;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.9%; Score 806; DB 2; Length 21 Best Local Similarity 68.9%; Pred. No. 5e-48; Matches 151; Conservative 28; Mismatches 40; Indels
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A,Reference number: PC4202; MUID:97082978; PMID:8964510
A,Accession: PC4203
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A;Residues: 1-219 <KWA>
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:g1594225; RIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;1-112/Domain: C region #status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accesion: PG203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.: Park, V.R.: Han
A,Status: preliminary
A,Anolocule type: mRNA
A,Residues: 1-219 «VAN>
A,FCROSS-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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68.0%; Pred. No. 4.3e-48;
tive 31; Mismatches 39;
                                                                                                                                                                                                           66.0%; Score 820; DB 2;
69.4%; Pred. No. 5.6e-49;
live 28; Mismatches 39
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                                                                                                                                                                                                        Query Match
Best Local Similarity 69.4*
Matches 152; Conservative
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Cispecies: Mus musculus (house mouse)
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
Cibate: 06-Jan-1996
Rikipp, B.; Becker, W.; Schlaak, M.
Submitted to the EMBL Data Library, November 1993
AiDescription: Combination of a defined specificity and desired isotype by cloning of an
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A,Molecule type: mRNA
A;Residues: 1-219 eKIP>
A;Residues: 1-219 eKIP>
A;Cross-references: EMBL: 227396; NID: 9416538; PIDN: CAAB1787.1; PID: 9416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                         81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SIPPSSEQLTSGGASVVCFLANFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPWTFGGGTKLEIKRADAAPTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180
0; Gaps
                                                                                                              1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF 60
                                                                           EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.1%; Score 796; DB 2;
68.9%; Pred. No. 2.4e-47;
iive 26; Mismatches 42
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
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R, Allam, M.A.; Hara, Y.; Hosepain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A, Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A, Reference number: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: A23746
R; Leoni, U.; Ghiso, U.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A; Fitele: They primary structure of the Fab fragment of protein KAU, a monoclonal immunogla, Reference humber: A23746; MUID:91131575; PMID:1993660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Homo sapiens (man)
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
                                                                                                                                                                        81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                    141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                117 FIFPPSDEQLKSGTASVVCLLNNFYFREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 VFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIK-RTVAAPS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
                                                                                            21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                    21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 876; DB 2; Length 215;
Pred. No. 8.5e-53;
                 73.1%; Score 908; DB 2; Length 215; 79.9%; Pred. No. 5.7e-55; Live 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                                                                                                                     SSTLTLSKADYERGHKVYACEVTHQGLSSPVTKSFNRGEC 215
                                                                                                                                                                                                                                                                                                                               201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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77.7%; Pred. No. o...
've 18; Mismatches ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain NIG93 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.7% Matches 171; Conservative
                              Local Similarity 79.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A23746
A; Status: preliminary
A; Molecule type, protein
A; Residues: 1-215 <LEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JE0243
                 Query Match
Best Local Simi
Matches 175;
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JE0243
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Ig Kappa chain - mouse (Species Mus authorise Mouse) (Species Mus authorise Musculus (house mouse) (Species) Mus authorius (Aboreseine) (Space 107-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000 (Space 107-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000 (Space 107-May-1995 #sequence Space Mouse 1994 (Space 107-May-1995 Moust 1994 (Moust 1994 Mouse 1994) (Moust 1994 Mouse 107-May-1996 Moust 1994 Mouse 107-May-1996 Moust 107-Moust 107-Moust 107-Moust 107-Moust 107-Moust 
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C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: J60241
R;Ailm, M.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T. submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 FIFPPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVLTQSPDFLAVSLGERATINCKSSQSVLY-NSKNFLAWYQQKPGQ-PKLLIW-ANVRE 57
                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                           21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                                                                                                    DB 2; Length 215;
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A;Residues: 1.2mc.4al..
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                           25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 238
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                                                                                                                                                                                             Query Match
69.2%; Score 860; DB 2
Best Local Similarity 78.4%; Pred. No. 1e-51;
Best Local Similarity 78.4%; Pred. No. 1e-51;
Conservative 18; Mismacches
C;Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
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OM protein - protein search, using sw model

March 29, 2003, 09:06:24; Search time 10.7265 Seconds Run on:

(without alignments)
2141.995 Million cell updates/sec

1 MSLPAQLLGLLLCVPGSSG.........EVTHQGLSSPVTKSFNRGEC 239 US-09-758-173-6 1242 Title: Perfect score: Seguence:

283224 segs, 96134422 residues Gapop 10.0 , Gapext 0:5 Searched:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:* pir2:* pir3:* PIR 73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		de			SUMMAKIES	
Result No.	Score	Query Match	Length	DB		Description
1	915	73.7	215	: ~	JE0244	Iq kappa chain NIG
7	806	73.1	215	7	JE0242	chain
e	876	•	215	~	JE0243	
4	860	69.2	215	~	A23746	
'n	841.5		216	N	JE0241	
9	820	0.99	219	~	S52028	
7	807	65.0	219	~	PC4203	
8	806	64.9	219	~	S16112	kappa
6	796	64.1	219	7	S38865	kappa
10	795	64.0	217	~	S42772	
11	770	62.0	225	~	JL0029	
12	765.5	61.6	240	~	S06084	kappa chain
13	723.5	58.3	220	7	A31790	kappa chain
14	702	56.5	225	7	S37484	Ig kappa chain - m
15	694.5	55.9	218	~	S68241	Ig kappa chain V r
16	688.5	55.4	214	N	S68212	Ig kappa chain (Ma
17	688.5	55.4	218	~	JC5810	noclona
18	687.5	55.4	234	~	S14237	Ig kappa chain pre
19	989	55.2	197	C1	829593	Ig kappa chain (WM
20	684.5	55.1	234	~	801320	kappa
21	680	54.8	230	~	S33161	kappa chain
22	662.5	53.3	210	~	A56169	kappa
23	644	51.9	235	~	825058	
, 24	617	49.7	178	~	PT0219	kappa
25	599	48.2	135	~	S52059	
26	572		229	~	A20969	kappa
27	565.5	45.5	140	7	S22658	chain
28	552	44.4	133	~	S23230	kappa chain
29	552	44.4	133	7	2	NVK protein p

Ig kappa chain V-J	Ig kappa chain pre	Ig kappa chain V r	Ig kappa chain C r	Ig kappa chain V r	Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain V r	Ig kappa chain - h	Ig lambda-like cha	Ig kappa chain - h	Ig kappa chain - h	Ig kappa chain - h	Ig kappa chain C r	Ig kappa chain pre	anti-digoxin trans
S40357	K2HURP	840324	K3HU	S22902	840342	A24452	S26882	S40373	A49633	S40312	S40322	S40355	A37927	PL0106	PH0106
~	-	N	-1	7	2	,-4	~	~	~	~	~	N	N	~	~
136	133	133	106	142	135	133	132	128	238	126	132	131	66	144	132
44.4	44.3	44.2	44.1	44.1	43.6	43.3	43.2	43.0	42.9	42.2	41.9	41.8	41.3	41.1	40.9
۰.	550	549	548	548	541	538	537	534	533	524	520	519.5	513	510.5	508.5
25,															

ALIGNMENTS

Fighting M. M.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te submitted to JIPID November 1998
A; Description: A new subgroup of k type light chains (vkV) identified in cases of AL amy)
A; Reference number: JE0243
A; Reference number: JE0244
A; Redesence number: JE0244
A; Molecule type: protein
A; Residues: 1-215 cALI:
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-99/Domain: immunoglobulin homology <IMM> C;Species: Homo sapiens (man) C;Date: 05-Dec_1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 Ig kappa chain NIG2 precursor - human RESULT 1

6; Gaps Query Match 73.7%; Score 915; DB 2; Length 215; Best Local Similarity 80.9%; Pred. No. 1.9e-55; Matches 178; Conservative 19; Mismatches 17; Indels

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21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80 ò

81 SGVPDRFSGSGAGTDFTLKISAVEABDVGVYFCGQGTRTPP-TFGGGTKVEIKRTVAAPS 139 ò g

g

176 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215 200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239 ò

RESULT 2 JE0242

Decays chain NIG26 precursor - human Cispecies: Homos appiens (man) Cispecies: Mankli, XI, Yamakli, XI, Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T. submitted to JIPID, November 1998 A; Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult A; Recession: JED243 A; Molecule type: protein A; Accession: JED243 A; Molecule type: protein Cispecial (mannoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology <IMM>

Search completed: April 6, 2003, 06:25:19 Job time : 37.7832 secs

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1734 TAA 1736
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                                                                                                               GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Choiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Holmes, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
APPLICANT: Hassen, Timochy W.
TITLE OF INVENTION: Recombinant IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STRRET: Pends of Prussia
COUNTRY: USA
IL19406-0939
COUNTRY: USA
INPERING OF SYSTEM: PC-DOS/MS-DOS
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/940,371
FILLING DATE: WALLED AND AND ALS.
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-940-371-50
: Sequence 50, Application US/08940371
: Patent No. 5851525
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APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: 950282
TELEPHONE: 610 270-5024
TELEPHONE: 610 270-5024
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 5703 base pairs
TYPE: nucleic acid
STANDEDNESS: double
            US 08/363131
                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-940-371-50
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Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
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STRANDEDNESS: double
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
                                                                                                                                                                                                                                                                                                                   Query Match 68.0%; Score 489.4; DB 1; Length 5703; Best Local Similarity 80.8%; Pred. No. 6.4e-135; Matches 584; Conservative 0; Mismatches 136; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-667-769A-50
; Sequence 50, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Amee, Robert S.
; APPLICANT: 'Appelbaum', Edward R.
                                                                                                                                                                             ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-470-110A-50
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 5703 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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1134 ATCAACTGCAAGAGCTCTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCC 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG 60
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APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant ILS Antagonists Useful in TITLE OF INVENTION: Treatment of ILS Mediated Disorders NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%; Score 489.4; DB 1; Length 80.8%; Pred. No. 6.4e-135; ive 0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
                                                                                        STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-UNN-1995
FRIOR APPLICATION NUMBER: US 08/467420
FILING DATE: 06-UNN-1995
FRIING DATE: 06-UNN-1995
FRIING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A.
REGIGTRATION NUMBER: 34,028
REGIGOMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEPAX: 610-270-5090
INFORMATION: 600-270-5090
INFORMATION: 600-270-5090
SEQUENCE CHARACTERISTICS:
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1614 CTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC
                 CCTCCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCT
                                            GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant ILS Antagonists Useful in TITLE OF INVENTION: Treatment of ILS Mediated Disorders NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P. O. Box 1539-UW2220 CITY: King of Prussia STATE: Pennsylvania COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SUffer, Jeffrey A.
REGISTRATION NUMBER: 34.028
REFERENCE/DOCKET NUMBER: P50282
TELEPHONE: 610 270-5024
TELEPHONE: 610 270-5090
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5693323
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-470-110A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5703;
                   APPLICANT: Charken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant ILS Antagonists Useful in TITLE OF INVENTION: Treatment of ILS Mediated Disorders NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
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Best Local Similarity 80.8%; Pred. No. 6.4e-135;
Matches 584; Conservative 0; Mismatches 136;
                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSE: Intellectual Property STREET: P. O. Box 1539-UW2220 TTTY: King of Prussia STATE: Pennsylvania
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FILING DATE:
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SULCON, JOÉFERY A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELEPHONE: 610 270-5024
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5024
TELEFAX: 610 270-5026
TELEFAX: 610 270-5026
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Appelbaum, Edward R.
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STRANDEDNESS: double
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PRIOR APPLICATION DATA:
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APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shabrokh, Zahra
APPLICANT: Zapata, Gerardo A.

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                                                                                                                                                                            CTCACGTTCGGTGCTGGGACCAAGCTGGAACTGAAACGGGCTGTTGCTGCACCAACTGTA 429
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                                                                                                                                       TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGCCAGGGACAGATTTCACACTGAAAATC 300
                                                                                                                                                                                                                                                         301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/234,340A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/09234340A
Patent No. 646632
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DNA way
CITY: South San Francisco
STATE: California
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STREET: 1 DNA WAY
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MEDIUM TYPE: 3.5 incl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TCTGGGGTCCCCAGACTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAGGATC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.1%; Score 519.2; DB 4; Length 729;
86.7%; Pred. No. 4.4e-144;
tive 0; Mismatches 88; Indels 0
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B. B. B. REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELECHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-467-420A-50
i Sequence 50, Application US/08467420A
i Patent No. 5683892
i GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 86.7
Matches 572, Conservative
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550 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFIMARE: WITHGALL (GENERICEDIN)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-011-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
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FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R-
TELECOMMUNICATION:
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CITY: SOUTH SAN Francisco
STATE: California
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 1 DNA MAY STREET: 1 DNA MAY CITY: South San Francisco
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                                                                                                                                                                                                              CUONIVER: USAN
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Winbearin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION: ROCHMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R3-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMPUTER: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-09-026-985-41
                                                                                                                                                                                                       USA
                                                                                                                                                                                                       COUNTRY:
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RESULT 10
US-09-121-952A-41

US-09-121-952A-41

Sequence 41, Application US/09121952A

Patent No. 645835

GENERAL INFORMATION

APPLICANT: Generiech, Inc., Heei, Vanessa

APPLICANT: Leong, Steven R.

APPLICANT: Bahrokh, Zahra

APPLICANT: Sapara, Leonard G.

APPLICANT: Sapara, APPLICANT: Sapara, Inc., METHON B.

TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS: 72

ADDRESSE: Generiech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                   670 GTCACCCCATCAGGGCCTGAGCTCGCCGGTCACAAGAGGGCTTCAACAGGGGAGAGAGTGTTAA 729
                                                                                                                   661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAAGAGTGTTGA 720
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Sequence 41, Application US/09026985; Patent No. 6133426; GENERAL INFORMATION:
APPLICANT: Genealez, Tania R.,
APPLICANT: Leong, Steven R.
        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REFERENCE/DOCKET NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELEPHONE: 650/225-530
TELEPHONE: 650/255-530
TELEPHONE: 650/352-9881
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDRESS: Double
                                                                                                                                                                                                                     ; TOPOLOGY: Linear
US-08-804-444A-41
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US-09-026-985-41
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                                                                 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTGGAGAGCCGGCCTCC 120
                                                                                             70 GATATCGIGATGACACAGACACCACTCTCCCTGCCTGTCAGTCTTGGAGATCAGGCCTCC 129
                                 Gaps
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US-08-804-444A-41

Sequence 41, Application US/08804444A

Patent No. 6117980

GENERAL INFORMATION:

APPLICANT: Genzalez, Tania N

APPLICANT: Leong, Steven R.

APPLICANT: Leong, Leonard G.

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSE: Generech, Inc.

STREET: 1 DNA MAY
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0
DB 3; Length 729;
                               Indels
Score 519.2; DB 3;
Pred. No. 4.4e-144;
0; Mismatches 88;
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ZIP: 94.080
COMPUTRY READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
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STATE: California
Query Match
Best Local Similarity 86.7%;
Matches 572; Conservative (
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                                                                             61 GAAGTIGIGAIGACICAGICICCACIGICCCTICCCAICACACCIGGAGAGCCGGCCTCC 120
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                                                                                                          Gaps
                                                                                                                                                                                        250 TCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAGGATC
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                                           Indels
Query Match 72.1%; Score 519.2; DB 3; Best Local Similarity 86.7%; Pred. No. 4.4e-144; Matches 572; Conservative 0; Mismatches 88;
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REFERENCE/DOCKET NUMBER: P: TELECOMMUNICATION INFORMATION TELEPHONE: 650/225-5330 TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 41 SEQUENCE FRARACTERISTICS: LENGTH: 729 base pairs TYPE: Nucleic Acid STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
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RESULT.

US-08-491-334A-55

Sequence 55, Application US/08491334A

GENERAL INFORMATION:

APPLICANT: Kabakoff, Rhona C.

APPLICANT: Kabakoff, Rhona C.

APPLICANT: Macre, Mark W.

TITLE OF INVENTION: Disorders and Asthma

TITLE OF INVENTION: Disorders and Asthma

TITLE OF SEQUENCES: 58

CORRESPONDENCE: 58

CORRESPONDENCE: 58

CORRESPONDENCE: ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GATATCGTGATGACACAGACACCTCTCCCTGCTGAGTCTTGGAGATCAGGCCTCC 129
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                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE STILEN: E-DOS/US-DOS SOFTWARE WINPARIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/39611
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNESY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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361 CCCACTITICGGCGGAGGGACCAAGGIGGAAAICAAACGIACGIGGCIGCACCAICIGIC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA
ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION NUMBER: 60/074,330
FILING APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 12-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
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TCTGGGGTCCCGGACAGATTCAGCGGCAGTGGGGCAGGGACAGATTCACACTGAAAATC 300
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86.7%; Pred. No. 4.4e-144;
11ve 0; Mismatches 88;
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,851A
FILING DATE: U-ARR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                          874P1-4
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1489
TELEFAX: 415/552-9881
                                                                                                                                                                                                                                                                                                 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 86.7
Matches 572; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Patent No. 5707622
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Rebert, Carcioline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 549
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                                                                                                                                                          70 GATATCGTGATGACACAGACACTCTCCCTGCCTGTCAGTCTTGGAGATCAGGCCTCC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360
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                                                                               ;
0
                                          Length 729;
                                                                               88; Indels
                                   Query Match 72.1%; Score 519.2; DB 1; Best Local Similarity 86.7%; Pred. No. 4.4e-144; Matches 572; Conservative 0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-396-851A-55
US-08-398-611A-55
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310 AGCAGAGTGGAGGCTGAGGATCTGGGACTTTATTTCTGCTCTCAAAGTACACATGTTCCG 369
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34,659
ER: P0874P1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 729 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415/952-9881
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US-08-398-611A-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TACCTGCAGAAGCCAGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GAAGITGIGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GATATCGTGATGACACAGACACTCTCCCTGCCTGTCAGTCTTGGAGATCAGGCCTCC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                     US-08-398-612A-55
Sequence 5:5, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
PAPPLICANT: Describut, Claire M.
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: APPLICANT: Ann. Kyung Jin
APPLICANT: Hebery Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/30864
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/30864
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
RESISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: SE: SEQUENCE CHARACTERISTICS: LENGTH: 729 base pairs TYPE: Nucleic Acid STRANDENESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 86.7
Matches 572; Conservative
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Patent No. 5702946
Patent No. 57
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MEDITARIES READABLE FORM:
MEDITARIES READABLE FORM:
MEDITARIN TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION UNGRER: US/08/398,611A
RPPLICATION WURBER: US/08/398,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION OF 424
PRIOR PAPLICATION DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
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86.7%; Pred. No. 4.4e-144;
ative 0; Mismatches 88;
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/398,613A FILING DATE: 01-MAR.1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR.1994
ATTORNEY.AGENT INPORMATION: NAME: Fitts, Renee A. REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 35,136
REGISTRATION FOR SEQ ID NO: 55:
SEQUENCE CHRACATERISTICS:
LENGTH: 229 bases
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Best Local Similarity 86.73
Matches 572; Conservative
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STRANDEDNESS: single
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APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-1L-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                  61 GAAGITGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120
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                   Pred. No. 2e-203;
0; Mismatches 0; Indels
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COMPUTÉR READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-398-613A-55
Sequence 55, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
                   100.08;
                Best Local Similarity 100.
Matches 720; Conservative
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPACIBLE
OPERATUR: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
US-09-335-697B-16
US-08-276-852-152
US-08-899-575-152
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-899-575-156
US-08-276-852-170
US-08-899-575-156
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                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-487-550-5

Sequence 5, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:
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STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
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MOLECULE TYPE: peptide
FEATURE:
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CITY: Alexandria
STATE: VA
COUNTRY: USA
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LOCATION: 1..72
FEATURE:
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LOCATION:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/6A_COMB.seg:*
/cgn2_6/ptodata/1/ina/6B_COMB.seg:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
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Compugen Ltd.
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US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-50
US-08-467-420A-50
US-08-467-769A-50
US-08-940-371-50
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US-08-677-69A-50
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                 GenCore version
Copyright (c) 1993 - 2003
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                                                                                              nucleic search, using sw model
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Maximum Match 1008
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Maximum DB seq length: 200000000
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Match Length
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Db 1401 GAGGTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1457

Search completed: April 6, 2003, 01:56:13 Job time : 4520.08 secs

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/Organisma-Homo sapiens"
/db xref="taxon.9606"
/cell_line="human /mouse (NS-0) hetero-hybridoma cell line
ESD-1 (THERAD 03)"
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TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYLCNNHKRSNTKVDKKVFPRSCDKTHTCPPCPAFELLGGESVFLFPPRKDT
LHQPWRLNGYTCVVDVSHEDFEVKTRYVDGVEVHNAKTKPREGYNSTYRVVSVLTV
LHQPWLNGKRYKCKVSNYALPAIEKTISKAKGQPREPQYYLLPPSKDELTKNOVSKLT
CLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFS
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GFAYSSFWMHWVRQAFGRGLVWVSRINPDGRITVYADAVKGRFTISRDNAKNTLYLQM
                                                                                                                     Direct Submission
Submitted (03-SEP-1997) T. Paterson, National Science Laboratory,
Scottish Nat. Blood Transfusion Service, 12 Bristo Place,
Edinburgh, EH1 IEZ, Scotland, UK
Cell line reference McCann Carter M.C. et al (1993), Transfusion
Medicine, 3, 187-194.
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/gene="IgGIK"
/product="immunoglobulin kappa heavy chain variable
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36. .1457
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1624)
Paterson, T., Innes, J., McMillan, L., Downing, I. and Carter, M.C.
Variation in 1gG1 heavy chain allotype does not contribute to differences in biological activity of two human anti-Rhesus (D) monoclonal antibodies
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lisc_mgc@nhgri.nih.gov
lisc_mgc@nhgri.nih.gov
ttherDy,K.D., Becketrom-Sternberg,S.M.,
tesl.ey,R.W., Boulfard,G.G., Brinkley,C., Brooke,S.,
lan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
lan,X., Gupta,J., Mastrian,S.D., McCloskey,J.C.,
1., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
190n,R., Snyder,B., Stantripop,S., Thomas,P.J.,
ucchand,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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43)
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ht: Louis Staudt
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E 2 (bases 1 to 1631)

Submitted (04-JUL-202) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Direct Submission

L Submitted (04-JUL-202) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kausa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

Construction: Helix Research Institute of HRI) (supported by Japan

Key Technology Center etc.); 5' & 1'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; Olone Selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

RAB; HRI and HRI and RAB.
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/ DECOLOR = 10 = "BAC04926.1"

/ DECOLOR = 10 = "BEFGLSWLFLVAILKGVQCEVELVESGGGLAQPGGSLRLSCEAS

/ LTAINSLAID = "BEFGLSWLFLVAILKGVQCEVELVESGGGLAQPGGSLRLSCEAS

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SGGTAALGCLWKDYFPEPVVSWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSL

GYQTYLCOWNHRPSVTKVDKKVEPRSGDKTHTCPPCPAPELLGGPSVFLFPPKROTH

MISRTPEVTCVVVDVSHEDDEVKFWWYDGVEVHNAKTKRPEEQYNSTYRVVSVLTVL

HQDWLAGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRBELTKNQVSTTC

LVKGFYPSDIAVERBSGNGOPENVYKTTPPVLDSDGSFFLYSKLTVDKSRWQGGNVFSC

SWMHEALHNHYTQKSLSLSPGK"
                                                                                                                                                                                                                                                                                                                                     AK097010 1631 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ39691 fis, clone SMINT2010672, highly similar to Homo sapiens mRNA for immunoglobulin lambda heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Fukuzumi, Y., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagateuma, M., Murakawa, K., Kanchori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                           1382 CTCACCGTGGACAAGAGGAGGTGGCAGCAGGAGAACGTCTTCTCATGCTCCGGTGATGCTT 1441
                                                                                                                      1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
                                                                                                                                                        1442 GAGGGTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK097010.1 GI:21756642
oligo capping; fis (full insert sequence).
Homo sapiens small intestine cDNA to mRNA, clone_lib:SMINT2
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/clone lib="SMINT2"
/note="cloning vector: pME18SFL3"
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/db_xref="taxon:9606"
/clone="SMINT2010672"
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KEYWORDS

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			GACCCTGAGGTCAAGTTCA 	CACCAGGACTGGCTGAATG CACCAGGACTGGCTGAATG CACCAGGACTGGCTGAATG CCCCCCATCGAGAAAACCA GCCCCCATCGAGAAAACCA	ACCTIGCCCCATCCCGGG ACCTGCCCCCATCCCGGG AAAGGCTTCTATCCCAGCG	AACTRCAGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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Homo sapiens cDNA FLJ25951 fis, clone SYN0365, highly similar to AKO98817 GI:2175001

AK098817 LOCUS DEFINITION

RESULT 12

ACCESSION VERSION

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/trainlation="MREGLSWIPLVAILKGVQCBVQLLDSGGGLVQPGGSLRLSCAAS
GETFERSAMSWVRQAFGKGLEWVSSTTASGSDTYDADFVGRFTISRDNSRWTLYLQM
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SGGTAALGCLVKDYFPEPVYSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSS
GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAFELLGGPSVFLFPPKKDTL
MISTPEPVTCVVVDVSHEDPEVKFWYVDGVSVHNATKFRREEGYNSTYRVVSVLTVL
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LVKGFYPSDTAVEWSSNGQDENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGGNVFSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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Sugano, S. and Suzuki, Y.
Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (08-UIL-2021) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ins.u-tokyo.ac.jp, Tel:81-3-5449-5286,
oligo capping; fis (full insert sequence).
Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN
clone:SYN00365.
                                                                                                                                                                                                             Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watenabe, S., Ishida, S., Ono, Y., Horuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, Y., Kawamura, Mayami, Y., Ishi, R., Otsuki, T., Sato, H., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0; Mismatches 118; Indels 18; Gaps
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/note="cloning vector: pME18SFL3"
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/db_xref="GI:21758945"
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                      Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.o.]p, Tel:81-438-52-3975, Fax:81-438-52-3986)

NBDO human cDNA sequencing project supported by Ministry of

Boconomy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Hell:Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 ATGGAGTTGGGGCTGTGCTGGGTTTTTCCTTGTTGCTATTTTAAAAGGTGTCCAGTGTGAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGCAGTCTCTGGGTTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA
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      and Yamamoto, J.
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Best Local Similarity 90.0
Matches 1294; Conservative
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ORIGIN
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Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                  958 ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1317
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780 ACCAAGGIGGACAAGAGTIGAGCCCAAAICTIGIGACAAAACTCACACATGCCCACCG 839
                                                                                        900 GACACCCTCATGATCTCCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGAGCCAC
                                                                                                                                                                                                                                                                                                GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
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Homo sapiens shymus cDNA to mRNA, clone_lib:THYMU1
clone:THYMU1000554.
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AK097859.1 GI:21757751
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2 (bases 1 to 1633)
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Length 1633;

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RESULT 11 AK097859

ACCESSION VERSION

KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS REFERENCE

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NVFSCSVMHEALHNHYTQKSLSLSPGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
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                                                                                                                                                                                                                                                                         heavy chain constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC
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|TGTGCAGCGTCTGGATTCACCTTCAGTAATATGGCATGCACTGGGTCCGCCAGGCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 GGTCGGTGGGTACGATATACTACGTGACTACTATCGGATACTACTTTGACTACTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTICCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                 Length 1673;
                                                                                                                                             /product="immunoglobulin lambda heavy chain"
123. .509
                                                                                                                                                                                                                                                                                                                                                            Score 1184; DB 9; Length 1
Pred. No. 7e-230;
0; Mismatches 130; Indels
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Matches 1301; Conservative
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Submitted (03-SEP-1997) T. Paterson, National Science Laboratory,
Scottish Nat. Baod Transfusion Service, 12 Bristo Place,
Edinburgh, EH1 1EZ, Scotland, UK
Location/Qualifiers
1. 1673
/ Organism="Hono appiess"
/ db xref="taxon:9606"
/ cell line="human /mouse (NS-0) hetero-hybridoma cell line
LHM70445.3 (THERAD 06)"
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Constant region; 1gG1; immunoglobulin; lambda heavy chain; variable
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GFTEGNYGMHWYRQAEGKGLEWVAAIWYDGSNKYYADSVKGRFTISRDNSKNTLYMQM
SERABUFTAVYYCARRGGRWYRYTYTTIGYYPPYWGGATLYWSAAGTKGESVFPLAP
SSKGTSGGTAALGCIVKDYPPERPYTSMNSGALTSGVHTFPAVLQSSGLYSISSVVTV
PSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCTAPELLGGPSVFLFPPR
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKRREEQYNSTYRVVS
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 1673)
Paterson, T., Innes, J., McMillan, L., Downing, I. and Carter, M.C.
Variation in IgG1 heavy chain allotype does not contribute to
differences in biological activity of two human anti-Rhesus (D)
monoclonal antibodies
Immunotechnology 4 (1), 37-47 (1998)
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1112 · CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1171
                                                            1172 GCCCCCATCGAGAAAACCATCTCCAAAGGCAAGCCAGCCCGGAGAACACAGTGTAC 1231
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'protein id="CAA75032.1"
'db xref="GI:2765425"
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TITLE
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0; Mismatches 134;
     Similarity 90.0%;
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/cransi_table=11
/producf="heavy chain antibody 3D6"
/protein_id="CAA01549.1"
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                                                                                                                                                   GCCCCCATGGAGAAACCATCTCCAAAGGCAAAGGCAGCCCGGAGAACCAGGTGTAC
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DEFINITION ACCESSION VERSION KEYWORDS

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BETINITION Sequence 1 from Patent W00188132.
ACCESSION AX419496
VERSION AX419496
NUMBERION
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VKGFYEDILAUGNSSNNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 42 Row: o Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AIGGGTIGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 GGCACCCTGGTCACTGTCTCCTCAGCCTCCAAGGCCCCATCGGTCTTCCCCCTGGCA
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Pred. No. 2.5e-230;
0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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/clone lib="NIH MGC_113"
/lab host="DH10B-R"
/note="Vector: pOTB7"
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/organism="Homo sapiens"
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Matches 1298; Conservative
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Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.
BC024289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1630)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1059 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGGTCTCCAACAAAGCCCTCCCA 1118
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                                  AACTACAAGACCACGCCTCCCGTGCTGGAACTCCGACGGCTCCTTCTTCCTCTACAAGAAG
     GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
                                                                                                              AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG
                                                                                                                                                    999 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTGCTCTG
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Contact: MGC help desk
Email: cgapbs.ramail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@Dogge.bc.ca
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Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m marker), clone MGC:31937 IMAGE:4851063, mRNA, complete cds.
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NSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: i Column: 16 This clone was selected for the following selection criteria: Hexamer frequency ORF passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1679)
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                                     1389 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGGGGGAACGTCTTCTCATGCTCC 1448
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Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/clone lib="NIH MGC 48"
/lab_host="DH10B-R"
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/clone="MGC:31937 IMAGE:4851063"
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/organism="Homo sapiens"
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KGFYPEDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSV
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                                                                                                                                                                                                                                                                                                                   82.7%; Score 1188.2; DB 9; Length 1679;
                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.9e-231;
0; Mismatches 113; Indels
                                                                                                                                                                                                             291 t
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.5%;
Matches 1300; Conservative
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471 548 531 608 591 668 651 728 711 788 771 848 831 908 891 968

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CAGGIGIACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1268
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   GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGGCAGCCCCGAGAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 Argeagtreseacreaecresarrrrecrirreserarraaaaserereaerereaa 134
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/codon_serart=1
/prodict="Similar to immunoglobulin heavy constant (G3m marker)"
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help deak
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
TobN Library Preparation: Rubin Laboratory
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1189.2; DB 9; Length 1666; Pred. No. 6.2e-231; 0; Mismatches 123; Indels 15;
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db.xref="Laxon:9606"
/clone="MGC:12848 IMAGE:4108411"
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/note="Vector: pOTB7"
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1666 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m marker), clone MGC:12848 IMAGE:4308411, mRNA, complete cds.
BC006402.1 GI:13623574
MGC.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Direct Submission
Direct Submission
Submitted (09-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1318 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1377
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                                                             ACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACCG
                                                                                                                                                                           ACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAAAAAACTCACACCG
                                                                                                                                                                                                                                                                                                TGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCCAAAACCCAAG
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                                                                                                                                                                                                                                                              ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGGCCCTC
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/ db xref="G1:1579222"
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/ tb xref="G1:15792"

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/product="Similar to immunoglobulin heavy constant gamma 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
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                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                           /tissue type="Spleen"
/clone_lib="NIH MGC_113"
/lab_host="DH10B-R"
                                                                                                                                                                                                 'note="Vector: pOTB7"
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	3750	3810	1147	3930	3990	1327	DD 4110 CTG	RESULT 4 BC014667 LOCUS	ACCESSION E	SOURCE FORGANISM	REFERENCE 1 AUTHORS STILLE	JOURNAL	COMMENT					FEATURES
Moce="cDNA"	Query Match Best Local Similarity 91.3%; Score 1219; DB 6; Length 7521; Best Local Similarity 91.3%; Pred. No. 5e-237; Matches 1307; Conservative 0; Mismatches 115; Indels 9; Gaps 1;	OY 7 IGGAGCCICATCTIGCICTICCTIGCGCTGTACGAGCGTGCCAGTGTGAGGTGCAA 66 Db 2739 TIGIGGCTGAACTGGATTTCCTIGTAACACTTTTAAATGGTAICCAGTGAGGTGAAG 2798	Qy 67 CTGGTGGAGTCTGGGGGGGGGGGGCCCCTGAGAGTCTCCTGTGCA 126 Db 2799 CTGGTGGAGGAGGAGGAGGGTTGGTACAGCCTGGGGGTTCTCTGAGTCTCTCTGTGCA 2858	Qy 127 GTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCAGGGAAG 186 Db 2859 GCTTCTGGATTCACCTTCACTACATACTACATGAGCTGGGTCCGCCAGCCTCCAGGGAAG 2918	QY 187 GGGCCGGAATGGGTAGGTTTCATTAGAAACGAACGGTGGGACAACAGAATACGCC 246 Db 2919 GCACTTGAGTGGTTGGTTTGATTAGAAAGCTAATGGTTACACAACAAGAGTACAGT 2978	Qy 247 GCGTCTGTGAAAGAGTCACCATCTCCAGAGATGATTCCAAAAGCATCGCCTATCTG 306 Db 2979 GCATCTGTGAAGGTCGGTTCACCATCTCCAGAGATAATTCCCAAAGCATCTCTATCTT 3038	OY 307 CAAATGAGCAGCCTGAAAATGAGGACACGGCGTCTATTACTGTACTACATCCTACATT 366	ON 367 TCACATTCTCGGGGTGGTGTCTCCTATGGAGGTTACTTCGAATTCTGGGGCGCCC 426	OY 427 CIGGICACCGICTCCCCAGCTAGCACCAAGGCCCAICGGTCTICCCCCTGGCACCCTCC 486	QY 487 TCCAAGAGCACCTCTGGGGCACAGGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 546 D 3210 TCCAAGAGCACCTCTGGGGGACACAGGGGCCCTGGGCTGGCT	Qy \$47 GAACCGGTGACGGTGCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 606 Db 3270 GAACCGGTGACGTGTGCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 3329	OY 607 GCTGTCCTACAGACTCTACTCCCTCAGAGGTGGTGACGTGCCCTCCAGC 666	OY 667 ACCTIGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGGCAGCAAGGAGGAAGGTG 726	Oy 727 GACAAGAAGCAGAGCCCAAATCTTGTGACAAAACTCACACACTGCCCACGTGCCCAGGA 786 	Oy 787 CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 846 Db 3510 CCTGAACTCCTGGGGAACCGTCAGTCTTCCTCTTCCCCCCCAAACCCAAAGCCCTC 3569	ON 847 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAGCCTGAGCCACGAAGACCCT 906	Oy 907, CAGGTCAAGTTCAACTGGTAGGACGGCGTGGAGGTGCATAATGCCAAGACAAGGCG 966 	Oy 967 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGGTCAGCGTCCTCACCGTCCTGCACCAG 1026

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USAR

CONTRACT: MGC help desk

Tissue Procurement: Dr. Mark Watson

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CABORA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

infoobges. Dr. ca

steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Letticial Hislao, Marrin Krzywinski, Retz Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prebhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasia wan den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.
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Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m
marker), clone MGC:23153 INAGE:4850078, mRNA, complete cds.
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Location/Qualifiers
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Mammallai: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1659)
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Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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DEFINITION
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                                               /clone="THYMU2017844"
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Patent: WO 0109303-A 1 08-FEB-2001;
VICAL INCORPORATED (US)
Location/Qualifiers
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1 (bases 1 to 7521)
Hermanson, G.G.
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GenCore version 5.1.3
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OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	April 5, 2003, 19:13:05; Search time 4509.08 Seconds (without alignments) 9274.790 Million cell updates/sec
Title: Perfect score; Seguence:	US-09-758-173-7 1437 1 ATGGGTTGGAGCCTCATCTTCCCTGTCTCCGGGTAAATGA 1437
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq	Minimum DB seq length: 0

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Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	AR108865	Sequence 7 from patent US 6113898.	AR108865	AR108865.1 GI:12825141		Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1437)	Ande	Human B7.1-specific primatized antibodies and transfectomas	expressing said antibodies	Pate
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LT 1 8865	ເກ	ILLIN	SSIO	NOI	ORDS	B	ORGANISM		RENC	AUTHORS	TITLE		JOURNAL
RESULT 1 AR108865	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ÓŖ		REFERENCE	AU	T		5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 203
144 PIFPPSDEQLKSGTASVVCLLANPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 EVWITQSPLSLPITPGEPASISCRSSQSLKHSNGDIFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gonzalez, Tania R.
APPLICANT: Gonzalez, Tania R.
APPLICANT: Deng, Steven R.
APPLICANT: Presta, Leongrand G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.4%; Score 936; DB 4; Length 242; Best Local Similarity 81.7%; Pred. No. 1.8e-74; Matches 179; Conservative 15; Mismatches 25; Indels
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                                                                                        204 SSTLTLSKADYEKHKVYACEVIHOGLSSPVIKSFNRGEC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R3-1
TELECHONIOI CHOORNATION:
TELEPHONE: 650/255-530
TELEFAX: 650/952-9831
INPORVATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYRE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                              Sequence 62, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
                                                                                                                                                                                              US-09-026-985-62
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Search completed: March 29, 2003, 09:17:41 Job time : 8.49182 secs

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56 YQQRPGQSPRLLIYGASTRATGVPPRFSGGGGGTEFTLFISSLQSEDFALYYCQQYKGWP 115
                                                                                                                                                                            116 LTFGGGTRVQIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 175
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      61 YOOKPGOPPRILIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                      121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gonzalez, Tania R. APPLICANT: Gonzalez, Tania R. APPLICANT: Leong, Steven R. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies CORRESPONDENCE: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 242;
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75.4%; Score 936; DB 3; Length 242
Best Local Similarity 81.7%; Pred. No. 1.8e-74;
Matches 179; Conservative 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DS/MS-DOS SOFFWARE: WinPatin (Genericch) SURRENT APPLICATION DATA: MS-1998 FILING DATE: 20-Peb-1998 FLIANG DATE: 20-Peb-1998 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 60/074,330 FILING DATE: 22-Jan-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/039,664 FILING DATE: 21-Feb-1997 ATTORNEY/AGENT INFORMATION: NAME: LOVE, Richard B: REGISCRATION NUMBER: 34,659 REFERENCE/DOCKT NUMBER: 91085R3-2 PRIOR AND NUMBER: 19109 REFERENCE/DOCKT NUMBER: 19109 REFERENCE/DOCKT NUMBER: 91085R3-2 PRIOR AND NUMBER: 19109 REFERENCE/DOCKT NUMBER: 91085R3-2 PRIOR AND NUMBER: 91085R3-2 PRIOR AND NUMBER: 91085R3-2 PRIOR AND NUMBER: 91085R3-2 PRIOR NUMBER: 91085R3-2 PRIOR AND NUMBER: 91085R3-2 PRIOR NU
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; Sequence 62, Application US/09027449
Partent No. 6025158
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: General STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 242 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: 3.5 inc
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US-09-027-449-62
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                                                                                                                                      61 WYQQKPGQPPKLLIFWASTRESGVPDRFSGSGFGTDFTLTISSLQAEDVAVYYCQQYFSY 120
                                                                                                       120 PPTFGGGTKVEIKKTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNAL 179
                                                                                                                                                                                                                                      180 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                     181 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09049672A

Batent No. 6135941

GENERAL INPORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 234;
75.6%; Score 939.5; DB 4; Length 77.0%; Pred. No. 8.3e-75; Live 23; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NERS: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39,132
FP. PF-0497 US
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 234 amino acids

; TYPE: amino acid

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: COLSUCT01

; CLONE: 2280869

US-09-049-672A-6
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SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 184; Conservative
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Best Local Similarity
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US-09-049-672A-6
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14. FIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSL 200

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60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                             21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 DIVMIQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNRF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSLPAQLIGLLILCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHS-NGDTFLS
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                                                                                                                                                                                                                                                                                                                                           78.6%; Score 976; DB 4; Length 242; llarity 84.5%; Pred. No. 5.6e-78; Conservative 16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.5%; Score 975.5; DB 4;
80.4%; Pred. No. 6.1e-78;
Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTONEX/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/OCKET WINBER: P1085R4
TELECOMUNICATION INFORMATION:
TELECHONE: 650/255-5530
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.49
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 185; Conserv
                                                                                                                                                                                                                                                                                                       US-09-234-340A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-301-593-36
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LENGTH: 240
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Sequence 42, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Shahrokh, Zahra
APPLICANT: Sapata, Gerardo A.
ITILE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                               78.6%; Score 976; DB 4; Length 242; 84.5%; Pred. No. 5.6e-78; Live 16; Mismatches 18; Indels
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APPLICATION NUMBER: US/09/234,340A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFRENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPACH 650/225-5530
TELEPACH 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 anino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 84.59
Matches 185; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                         US-09-121-952A-42
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-121-952A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 FIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Application antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Indels
                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,444A FILING DATE: 21-Feb-1997 CLASSIFICATION: 530 ATTOWNEY/AGENT INFORMATION: NAME: LOVE, Richard B. REGISTRATTON NUMBER: 91085 TELECOMMUNICATION INPORMATION: FELECOMMUNICATION INPORMATION: TELEPHONE: 650/225-530 TELEPHONE: 650/225-530 TELEPHONE: 650/952-9881 INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.6%; Score 976; DB 3; Best Local Similarity 84.5%; Pred. No. 5.6e-78; Matches 185; Conservative 16; Mismatches 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WinPatin (Genentech)
ADDRESSEE: Genentech, Inc.
                   T: 1 DNA Way
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 242 amino acids TYPE: Amino Acid
                                                              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-804-444A-42
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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| APPLICATION | PAPEL | 1999 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 |
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US-08-804-444A-42

Sequence 42, Application US/08804444A

Patent No. 6117980

GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids
TYPE: Amino Acid
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US-09-027-449-42
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Sequence 56, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
TITLE OF INVENTION: 109crders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ANDRESCOUR CALLED OF TABLESS:
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84.5%; Pred. No. 5.6e-78;
ative 16; Mismatches 18.
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/39611
FILING DATE: 01-MAR-1995
FILING DATE: 03-MAR-1995
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAMME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 14,559
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.5%
Matches 185; Conservative
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US-09-027-449-42
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Sequence 42t Application US/09027449 Parent No. 6025158 GENERAL INFORMATION: APPLICANT: GQTXAIEZ, Tania R.

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SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
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APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ZUENTINE READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
FILING APPLICATION DATA: APPLICATION NUMBER: 60/038,664
FILING DATE: 22-Jan-1998
RICHEN APPLICATION NUMBER: 60/038,664
RILING DATE: 21-Feb-1997
ATTORIEY/AGENT INFORMATION: NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 91085R3-2
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.6%; Score 976; DB 3; Best Local Similarity 84.5%; Pred. No. 5.6e-78; Matches 185; Conservative 16; Mismatches 18
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81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAFSV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 DIVMIQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNRF 83
                                                                                                                                                            APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
TITLE OF INVENTION: of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ANDRESCOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 242;
204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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Best Local Similarity 84.5%; Pred. No. 5.6e-78;
Matches 185; Conservative 16; Mismatches 18.
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genencech, Inc.
STREET: 460 Point San Bruno Blvd
STRYE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 incu, i...

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
PRICH APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-530
TELEPHONE: 415/25-530
TELEPROME: 290/31-7168
INFORMATION FOR SEG ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                          RESULT 5
US-08-398-611A-56
; Sequence 56, Application US/08398611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-398-611A-56
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US-08-491-334A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 DIVMIQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNRF 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.6%; Score 976; DB 1; Length 242;
84.5%; Pred. No. 5.6e-78;
tive 16; Mismatches 18; Indels
                                                                                                                                                                                                                                                  APPLICANT: Doesehuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Hebert, Caroline Alice
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SQUENCES: 58
CORRESPONDENCE ADDRESS:
                 201 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                          204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/38611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARG B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 90874P1
TELECHONIS. 415/255-5530
TELECHAR: 415/255-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Geneticch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                     Sequence 56, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.5*
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                          US-08-398-612A-56
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122 YRTFGRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 181
                                                                                                                                                                       180 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYERGHKVYACEVTHQGLSSPVTKSFNRGEC 239
                           60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                                                                                                                                                                                            QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                     120 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALIFORNIA
SURVE: CALIFORNIA
ZIP: 94040
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALIA (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIPICATION 3478
APPLICATION ON TAR
FILING DATE: 03-MAR-1994
FILING DATE: 03-MAR-1994
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          874P1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitts, Renee A.
REGIGTRATION UNDBER: 35,136
REFERENCE/DOCKET NUMBER: 874E
TELECOMMUNICATION: TELECOMMUNICATION: 415,525-1489
TELEFAX: 415,952-9881
TELEX: 910,371-7168
INFORMATION FOR SEQ ID NO: 56:
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LENGTH: 242 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-398-613A-56
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                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/07916098A
Sequence 56, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, MARGARET S.
AUTILE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
2
                    61 YQQKPGQPPRILIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGOGTRTP 120
                                                                                     PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                         181 SGNSQESVTEQDSYDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPIPTPGEPASISCRSSQSLKHS-NGDIFLS 59
                                                                                                                                                                   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEIGHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.7%; Score 978; DB 2; Length 241; Best Local Similarity 80.4%; Pred. No. 3.7e-78; Matches 193; Conservative 22; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/07/916,098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
PRPLICATION NUMBER: US/07/916,09
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amino acid
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Sequence 56, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-6 Monoclonal Antibodies for Treatment of Inflammatory I
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 SGVPDRPSGSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLFFGAGTKLELKRAVAAPTV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 28, Appl Sequence 1, Appli Sequence 1, Appli Sequence 15, Appl Sequence 153, App Sequence 153, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli

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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONCHY MONCHOUND ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B? 1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSLPAQLIGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSLPAQLIGILILICVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

Z191: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: Patent Decompatible

SOFTWARE: Patent Decompatible

CURSATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

CLEASTFICATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: TESKIN, RObin L.

REGISTRATION NUMBER: 35,030

REGISTRATION NUMBER: 35,030

REGISTRATION NUMBER: 35,030

TELEFONDICATION NUMBER: 012712-131

TELECOMMUTICATION INFORMATION:

TELEFAX: 703-836-620

TELEFAX: 703-836-620

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1242; DB 3;
100.0%; Pred. No. 3.1e-101;
tive 0; Mismatches 0;
US-08-804-444A-56
US-09-026-88-56
US-09-121-958-56
US-09-314-340A-56
US-09-301-593-28
US-08-852-215-1
US-08-869-971-1
US-08-812-586-16
US-08-89-975-153
US-08-899-975-153
US-08-899-975-153
US-08-899-975-153
US-08-899-975-153
US-08-137-13152-2
US-09-301-593-17
US-09-301-593-17
US-09-301-593-17
US-09-31-593-17
US-09-31-593-17
US-09-31-593-17
US-09-31-593-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: GOODANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria STATE: VA COUNTRY: USA ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-487-550-6; Sequence 6, Application US/08487550; Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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  Best Local Sim
Matches 239;
     Query Match
Best Local (
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42, Appl
36, Appl
60, Appl
62, Appl
62, Appl
62, Appl
62, Appl
51, Appl
51, Appl
51, Appl
51, Appl
                                                                                                                                                                            March 29, 2003, 09:06:24; Search time 8.49182 Seconds (without alignments) 828.100 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51,
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72,
72,
                                                                                                                                                                                                                                                                                                                                     1 MSLPAQLLGLLLCVPGSSG.......EVTHQGLSSPVTKSFNRGEC 239
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. /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*

. /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*

. /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*

. /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*

. /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*

. /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                              GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-487-550-6
US-09-398-612A-56
US-08-398-612A-56
US-08-398-612A-56
US-08-398-612A-56
US-08-398-612A-56
US-08-09-027-449-42
US-08-027-449-42
US-09-027-449-42
US-09-026-98-42
US-09-026-98-42
US-09-010-59-62
US-09-010-59-62
US-09-010-59-62
US-09-010-59-62
US-09-011-952A-62
US-09-011-952A-63
US-09-011-952A-51
US-09-011-952A-51
US-09-011-952A-51
US-09-011-952A-51
US-09-011-952A-51
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US-09-026-985-72
US-09-121-952A-72
US-09-234-340A-72
US-09-027-449-56
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-09-234-340A-72
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1242
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Match Length
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Perfect score:
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No.
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Gaps

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Length 239; Indels

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PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR PILING DATE: 2000-11-17
PRIOR PELING DATE: 2000-14,242
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR PILING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-19
PRIOR PELING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-10-20
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61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                       121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                      1 MSLPAQLIGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                       SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Length 244;
                       Indels
                Matches 209; Conservative
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PTZ53
CURRENT APPLICATION NUMBER: US/09/760,479
CURRENT FILING DATE: 2001-01-16
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 946

Sequence 658, Application US/09760479 GENERAL INFORMATION:

RESULT 15 US-09-760-479-658

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                                                                                                                                                                                                        87.8%; Score 1091; DB 26;
87.4%; Pred. No. 9.9e-85;
live 17; Mismatches 13;
Query Match
Best Local Similarity
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61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                 131 YTFGQGTKLEIKRTVAAPSVFIFPFSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 190
                                                                                                                                                                                                                                                                                                            121 PTFGGGTKVEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQ 180
                                                                                                                                                      Gaps
                                                                                                                                                                              1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                  181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                    16; Indels
                                                                                                                  86.4%; Score 1073; DB 21
87.0%; Pred. No. 3.8e-83;
tive 15; Mismatches 16
   2.0
                                                                                                                Query Match
Best Local Similarity 87.09
Matches 208; Conservative
; SOFTWARE: Patentin Ver. 2; SEQ ID NO 658; LENGTH: 262; TYPE: PRT; CRGANISM: Homo sapiens US-09-760-479-658
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Search completed: March 29, 2003, 09:34:12 Job time : 111.835 secs

PRIOR FILING DATE: 2000-06-28

PRIOR PLILAND DATE: 2000-07-11

PRIOR PLILAND DATE: 2000-07-11

PRIOR PLILAND DATE: 2000-06-14

PRIOR PLILAND DATE: 2000-06-14

PRIOR PLILAND DATE: 2000-07-26

PRIOR PLILAND DATE: 2000-07-26

PRIOR PLILAND DATE: 2000-07-12

PRIOR PLILAND DATE: 2000-07-14

PRIOR PLILAND DATE: 2000-07-17

PRIOR PLILAND DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 60/225, 686

PRIOR APPLICATION NUMBER: 60/225, 676

PRIOR APPLICATION NUMBER: 60/225, 677

PRIOR APPLICATION NUMBER: 60/225, 677

PRIOR PLILAND DATE: 2000-07-07

PRIOR APPLICATION NUMBER: 60/235, 270

PRIOR PLILAND DATE: 2000-09-14

PRIOR PLILAND DATE: 2000-09-14

PRIOR PLILAND DATE: 2000-09-17

PRIOR PLILAND DATE: 2000-09-17

PRIOR PLILAND DATE: 2000-09-27

PRIOR PLILAND DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/236, 369

PRIOR PLILAND DATE: 2000-09-29

PRIOR PLILAND DATE: 2

R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
R PILING DATE: 2000-09-29
R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/236,802 R FILING DATE: 2000-09-08

R APELICATION NUMBER: 60/229,509

R FILING DATE: 2000-09-05

R APELICATION NUMBER: 60/236,367

R FILING DATE: 2000-09-29

R APELICATION NUMBER: 60/237,039 APPLICATION NUMBER: 60/246,474 FILING DATE: 2000-11-08 APPLICATION NUMBER: 60/246,532 APPLICATION NUMBER: 60/249,207 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,245 FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,217
APPLICATION NUMBER: 60/249,217
APPLICATION NUMBER: 60/249,211 APPLICATION NUMBER: 60/249,215 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,264 APPLICATION NUMBER: 60/239,935 FILING DATE: 2000-10-13 APPLICATION NUMBER: 60/239,937 FILING DATE: 2000-10-13 APPLICATION NUMBER: 60/241,787 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/227,182 PILING DATE: 2000-08-14
APPLICATION WINBER: 60/235,836
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/230,438 FILING DATE: 2000-06-30 APPLICATION NUMBER: 60/225,266 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/237,037 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,040 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/240,960 APPLICATION NUMBER: 60/249,216 APPLICATION NUMBER: 60/249,210 FILLING DATE: 2000-11-17 APPLICATION NUMBER: 60/226,681 LICATION NUMBER: 60/225,759 APPLICATION NUMBER: 60/225,213 LICATION NUMBER: 60/215,135 APPLICATION NUMBER: 60/249,218 APPLICATION NUMBER: 60/249,213 APPLICATION NUMBER: 60/249,212 APPLICATION NUMBER: 60/249,244 FILING DATE: 2000-11-17 LICATION NUMBER: 60/225,214 FILING DATE: 2000-10-20 FILING DATE: 2000-10-20 FILING DATE: 2000-11-17 2000-08-14 2000-10-02 2000-08-22 LING DATE: 2000-08-14 2000-08-22 2000-09-06 FILING DATE: 2000-11-17 LING DATE: LING DATE: LING DATE: LING DATE: FILING DATE: LING DATE: ING DATE: PRIOR
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US-09-760-479-641
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US-10-206-008-641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLQKPGQSPRLLIXKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTPLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVŢHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: L chain of COTHER INFORMATION: humanized anti-Fas antibody US-09-046-351-82
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                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
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APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Nakahara, Kaori
APPLICANT: Vonehara, Shin
TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
FILE REFERENCE: 980125/HG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: JP HEI 9-67938
EARLIER FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PATENTI Ver. 2.0
SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Yonehara, Shin
ITLE OF INVENTION: HUMANIZED ANTI-HUMAN FAS ANTIBODY
FILE REFERENCE: 980125/HG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT FILING DATE: 1998-03-23
FARLIER FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PARLENT Ver. 2.0
SEQ ID NO 78
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                        89.6%; Score 1113; DB 14;
90.0%; Pred. No. 1.3e-86;
Live 9; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.4%; Score 1110; DB 14;
89.5%; Pred. No. 2.3e-86;
Live 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 78, Application US/09046351A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 89.5*
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.09
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-046-351-78
                                                                                                                                                                                                                                                                                                 FEATURE:
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61 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVP 120
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                                                                                                                                                                                                                                                               61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                 1 MRLPAQLIGILMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSKSLVHSNGNTYLHW
1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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US-09-760-479-641
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NOLICE: PTZ53
CURRENT APPLICATION NUMBER: US/09/760,479
CURRENT FILING DATE: 2001-01-16
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 946
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT235CIN

CURRENT APPLICATION NUMBER: US/10/206,008

CURRENT FILING DATE: 2002-07-29

PRIOR PELLING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-02-44

PRIOR FILING DATE: 2000-02-44
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87.4%; Pred. No. 9.9e-85;
tive 17; Mismatches 13; Indels
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Matches 209; Conservative
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ORGANISM: Homo sapiens
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61 YLQKPGQSPRLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVP 120
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                                                                                                                                                1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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                                                   Length 239;
                                                                                                    Indels
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
APPLICANT: Takahashi, Tohru
APPLICANT: Tohru
APPLICANT: Vonehara, Shin
TITLE OF INVENTION: HUWANIZED ANTI-HUWAN Fas ANTIBODY
FILE REFERENCE: 980125/HG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT PILING DATE: 1998-03-23
EARLIER APPLICATION NUMBER: JP HEI 9-67938
EARLIER FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 189
SOSTWARE: Patentin Ver. 2.0
                                                 89.9%; Score 1116; DB 14;
90.4%; Pred. No. 6.9e-87;
ive 8; Mismatches 15;
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ORGANISM: Artificial Sequence
                                                                                                  Matches 216; Conservative
                                                                         Local Similarity
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US-09-046-351-80
         US-09-046-351-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1242; DB 25; Length 239; 100.0%; Pred. No. 1.1e-97; ive 0; Mismatches 0; Indels 0;
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Harahashi, Tohru
APPLICANT: Nakahara, Kaori
APPLICANT: Nokahara, Shin
APPLICANT: Vonehara, Shin
TITLE OF INTENTION: HUWANIZED ANTI-HUWAN Fas ANTIBODY
FILE REFERENCE: 980125/HG
CURRENT APPLICATION NUMBER: US/09/046,351A
CURRENT FILING DATE: 1998-03-23
EARLIER PILING DATE: 1998-03-23
SARLIER FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.0
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: US 08/487,
RILING DATE: O7-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TERKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acids
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 239; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRLPAQLIGILMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSKSLVHSNGNTYLHW 60
                                                                          Gaps
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Query Match 89.6%; Score 1113; DB 14; Length 239; Best Local Similarity 90.0%; Pred. No. 1.3e-86; Matches 215; Conservative 9; Mismatches 15; Indels 0
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; Sequence 82, Application US/09046351A
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Sequence 6, Application US/10124905
GENERAL INFORMATION:
APPLICANT: Anderson. Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                  CIP: 2314
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 08/487,
FILING DATE: 0.-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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                                                Alexandria
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-124-905-6
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TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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GENERAL INFORMATION:
APPLICANT: Anderson. Darrell R.
APPLICANT: Anderson. Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMBN B7.1 AND/OR B7.2 PRIMATIZED FRANS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: INMUNOSUPPRESANTS"
NUMBERN OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE:* BURNS, DOANE, SWECKER & MATHIS
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                                                                                                                                                                                                                                    COUNTY: USA

ZIP: 22314

COUNTY: USA

ZIP: 22314

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/030,390

FILING DATE:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE:

APPLICATION NUMBER: 010-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                         CITY: Alexandria
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US-10-124-807-6
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REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
         Sequence 6, Application US/09948429B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 239; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                         ZIP: 22314
COMPUTER READABLE FORM:
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US-10-030-390-6
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                                                                                                                                                                  APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "O HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMANCEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSE: SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/758,173
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Pred. No. 1.1e-97;
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REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/487,550
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,556
FILING DATE: 07-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
                                                                                           RESULT 4
US-09-758-173-6
Sequence 6, Application US/09758173
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Matches 239;
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ADDITION: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL AND R 87.2 PRIVATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HARMCEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSLPAQLIGILILCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
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100.0%; Pred. No. 1.1e-97
iive 0; Mismatches 0
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APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: HEARD, CHERYL
TITLE OF INVENTION: INDEMN'IFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
TITLE OF INVENTION NUMBER: US(09/576,424
CURRENT APPLICATION NUMBER: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1242; DB 19; Length 239; Best Local Similarity 100.0%; Pred. No. 1.1e-97; Matches 239; Conservative 0; Mismatches 0; Indels 0;
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PRIOR APPLICATION NUMBER: PCT/US9/19906
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 08/146,361
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-0-10
PRIOR PLING DATE: 1996-0-11
PRIOR APPLICATION NUMBER: 08/487,550
PRIOR FILING DATE: 1995-06-07
SPIOR FILING DATE: 1995-06-07
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
SEQ ID NO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09576424 GENERAL INFORMATION;
                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH 239 amino acide TYPE: amino acid TOPOLOGY: linear
    703-836-2021
                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-576-424-6
TELEFAX:
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TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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100.0%; Score 1242; DB 17; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 239; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                  012712-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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REPERENCE DOCKET UNMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
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NEDIUM TYPE: FLORDY disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
CLASSIFTCATION
PRIOR APPLICATION NUMBER: US 08/487,550
FILING DATE: O-JUN-1995
S US-10-124-807-6
5 US-10-124-807-6
6 US-09-046-351-84
4 US-09-046-351-84
4 US-09-046-351-84
4 US-09-046-351-82
4 US-09-046-351-82
4 US-09-046-351-82
6 US-10-206-049-641
6 US-10-206-049-641
6 US-10-206-049-68
6 US-10-206-049-8
7 US-09-924-19-86-8
8 US-09-924-19-8-8
9 US-09-924-19-8
9 US-09-934-19-9
1 US-08-721-612D-19
1 US-09-731-85-11
1 US-09-731-85-11
1 US-09-731-85-11
1 US-09-731-85-11
2 US-09-73-85-11
3 US-09-73-85-11
4 US-10-031-355-12
4 US-10-031-355-13
5 US-09-972-656-106
8 US-09-972-656-106
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GENERAL INFORMATION:
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STATE: VA
COUNTRY: USA
7. 22314
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                                                                                                                                                                                                                                                                                                                              1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                            March 29, 2003, 09:10:32; Search time 109.835 Seconds
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1: /cgn2_6/ptodata71/paa/PSG_COMB.pep:*

2: /cgn2_6/ptodata71/paa/USOR_COMB.pep:*

3: /cgn2_6/ptodata71/paa/USOR_COMB.pep:*

4: /cgn2_6/ptodata71/paa/USOR_COMB.pep:*

6: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

7: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

8: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

9: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

10: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

11: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

12: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

13: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

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16: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

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28: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*

28: /cgn2_6/ptodata71/paa/USOR3_COMB.pep:*
                              GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-576-424-6
US-09-758-173-6
US-09-948-429B-6
US-10-030-390-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Sequence

Sequence 19, App. Sequence 4028, Ap

Sequence 641, Sequence 641, Sequence 658, Sequence 658,

Sequence 8 Sequence 8 Sequence 8

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61 SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIKRTVAAAPSV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                                                                                                                                                                                       75.0%; Score 932; DB 9; Length 219; 81.7%; Pred. No. 6.1e-40; tive 14; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 SSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SSTLTLSKADVEKHKVYACEVTHQGLSSPVTKSFNRGEC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/726,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-UL-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECHONE: 650/225-5530
TELEFAX: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.7
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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TOPOLOGY:
US-09-726-258-72
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                                                                                Query Match 75.0%; Score 932; DB 9; Length 242; Best Local Similarity 81.7%; Pred. No. 6.6e-40; Matches 179; Conservative 14; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                            204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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LENGTH: 242 amino acids
                     Amino Acid
                                                 US-09-726-258-56
                                  TOPOLOGY:
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Search completed: March 29, 2003, 09:38:39 Job time : 11.1622 secs

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81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                              84 SGVPSRFSGSGSGTDFTLTISSLQPEDFATYXCSQSTHVPLTFGQGTKVEIKRTVAAPSV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 FIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 203
                                                                                                                                                                                                                                                                                                                     21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                24 DIQMIQSPSSLSASVGDRVIITCRSSQSLVHGIGNTYLHWYQQKPGKAPKLLIYKVSNRF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Geneticch, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Shahrokh, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
ITILE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
                                                                                                                                                                                                                       75.3%; Score 935; DB 9; Length 242; 81.7%; Pred. No. 4.7e-40; ive 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,659
ER: P1085R4-1A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91095R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Geneticch, Inc., Heei,
APPLICANT: Koumenis, Iphigenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
                                                                  TOPOLOGY: 1.4-CA
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STATE: California
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
STREET: 1 DNA Way
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                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 203
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     24 DIQMTQSPSSLSASVGBRVTITCRSSQSLVHGIGETYLHWYQQKPGKAPKLLIYKVSNRF 83
                                                                                                                                                                                                                                                                                                                                                            21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13

US-09-726-258-51

SQUENCE 51, Application US/09726258

Publication No. US20030021790A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Sapata, Gerardo A.
TITLE OP INVENTION: ANTIBODY FRACHENT-POLYMER CONJUGATES AND
TITLE OP INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                 Query Match 75.4%; Score 936; DB 9; Length 242; Best Local Similarity 81.7%; Pred. No. 4.2e-40; Matches 179; Conservative 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 SSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
         P1085R4-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P1085R4-1A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME:\_LOVE, Richard B.
REFERENCE/DOCKET NUMBER: 91085R4.
TELECOMMUNICAFION INFORMATION:
REFERENCE/DOCKET NUMBER: P100:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
FELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acide
TYPE: Amino Acid
TYPE: Amino Acid
TYPE: Amino Acid
US-09-726-258-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genentech, Inc.
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STATE: California
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ADDRESSEE: Genentech
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNA Way
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CLASSIFICATION:
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APPLICANT: Teuzia, Katsunari
APPLICANT: Teuzia, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT PILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-03-30
PRIOR PELING DATE: 2001-03-30
PRIOR PELING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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Sequence 38, Application US/09859053

Patent No. US20020102658A1

APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauji, No. US20020103658A1uaki
APPLICANT: Hori, No. US20020103658A1uaki
APPLICANT: Hori, No. US20020103658A1uaki
APPLICANT: Hori, No. US20020103658A1uaki
APPLICANT: PINNENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
                                                                                                                      57 YQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 OSGNSOESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 236
WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                      61 YOOKPGOPPRILIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVBABDVGVYFCGO-GTRT 119
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                                                                                           120 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
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Patent No. US20020102658A1
GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
US-09-859-053-34
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Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Saharokh, Lahra
APPLICANT: Sapata, Gerardo A.
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: TO CONTRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 OSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOG/MG TATA
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/234,182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-38
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Best Local Sım
Matches 186;
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TYPE: PRT
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Sequence 50, Application WS. US203002257A1

GENERAL INPORMATION:

APPLICANT: Macina, Noberto A.

APPLICANT: Macina, Roberto A.

APPLICANT: Chen, Selyu

TILE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes

FILE REFERENCE: DEX.0214

CURRENT FILING DATE: 2001-07-20

FRIOR APPLICATION NUMBER: 60/219,834

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Patentin version 3.1

LENGTH: 228
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                                                                                                                                                                                                                                                             141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                       81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                            84 SGVPDRFSGSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLTFGAGTKLELKRAVAAPTV 143
                                                                                                                                                                                                                                                                                        144 FIFPPSSEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 SNRDSGV-PDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTV 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 DIVWTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNRF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                        78.6%; Score 976; DB 9; Length 242;
84.5%; Pred. No. 4.4e-42;
ive 16; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                            SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 242
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US-09-249-011A-22
Sequence 22, Application US/09249011A
Patent No. US20020176855A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.58
Matches 187; Conservative
                                    Query Match
Best Local Similarity 84.5
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-909-567B-50
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JS-09-726-258-42
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APPLICANT: CO, MAN SUNG APPLICANT: VASQUEZ, MAXIMILIANO

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Sequence 8, Application US/09799514

Sequence 8, Application US/09799514

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant
TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, and Ant
TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, and Ant
TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, and Ant
TITLE OF INVENTION: 1201-03-07

CURRENT APPLICATION NUMBER: PCT/USO0/23662

PRIOR APPLICATION NUMBER: 60/152,248

PRIOR APPLICATION NUMBER: 60/152,248

PRIOR APPLICATION NUMBER: 60/152,248

NUMBER OF SEC ID NOS: 19

SOFTWARE: Patentin Ver. 2.0
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7
                                                     APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GARY GARY S.
APPLICANT: ROIGHT, ANDREA
APPLICANT: RIGHT, ANDREA
APPLICANT: VELDMAN, DENISE
APPLICANT: VELDMAN, GERRTRUIDA M.
TITLE OF INVENTION: OF TREATMENT THEREWITH
FILE REFERENCE: 08702.0081-00000
CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCSQSYNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 960; DB 9; Length 239; 79.6%; Pred. No. 2.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches 27; Indels
CELNIKER, ABBIE CHERYL COLLINS, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 191; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 239
TYPE: PRT
ORGANISM: Mus sp.
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FEATURE:
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Patent No. US20020146750A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Honderikx, Maria P.G.

APPLICANT: Honderikx, Maria P.G.

TILLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 US

CURRENT APPLICATION NUMBER: US/09/822,698A

CURRENT FILING DATE: 2000-03-30

PRIOR PAPLICATION NUMBER: US 09/538,913

PRIOR PAPLICATION NUMBER: US 09/538,913

PRIOR PAPLICATION NOWER: US 09/538,913

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 112

SOFTWARE: Microsoft Word

SEQ ID NO 24

LENGTH: 220
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                                                                  GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.034, JDV
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PELING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR PELING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR PELING DATE: 2001-06-25
PRIOR PELING DATE: 2001-06-25
PRIOR PELING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 8
LENGTH: 239
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86.0%; Score 1068; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 1.2e-46;
Matches 207; Conservative 11; Mismatches 21; Indels
                         Sequence 8, Application US/09992600A
Publication No. US20030027161A1
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ORGANISM: artificial sequence
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ORGANISM: Homo sapiens
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; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-09-992-600A-8
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US-09-822-698A-24
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, OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-1gG1
US-09-822-698A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                    140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKR-TVAAPS 139
                                                                                                                                                                                                                                      1 EIVLIQSPLSLPVIPGEPASISCRSSQSLLHSNGYTYLDWYLQKPGQSPQLLIXSGSHRA 60
                                                                                                                                                                                                      21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                        DB 10; Length 220
                                                                               Query Match
Pest Local Similarity 87.7%; Pred. No. 6.3e-43;
Matches 193; Conservative 12; Mismatches 14; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
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APPLICATION NUMBER: 60/094003
FILING DATE: 4-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
RETERENCE/DOCKET NUMBER: 19108FR.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-5530
TELEPHONE: 650/25-5981
: INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHRACTERISTICS:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/09726258 Publication No. US20030021790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genentech, Inc.
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CITY: South San Francisco
STATE: California
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61 YHQKPGQSPQLLIYLGSNRASGVPDRPSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP 120
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                                                                                                                                                                                                                                                                                                                                                                       121 PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                      1 MSLPAQLIGLILLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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                                                                                                                              1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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GENERAL INCEMENTION:
GENERAL INCEMENTION:
APPLICANT: Tanaka, Hiroaki
ITILE OF INVENTION: HOMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.022.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PRIOR DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 8
LENGTH: 239
                    Query Match
100.0%; Score 1242; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 239; Conservative 0; Mismatches 0. Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/09924340; Publication No. US20030027248Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: 1..20
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US-09-924-340-8
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                 61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLMNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDDGVFFCGGGTRTP 120
                                                                                                                                                                                                                                                                                             1 MSLPAQLIGLILLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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                                                                                                                                                   Query Match
100.0%; Score 1242; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 3.1e-55;
Matches 239; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & WATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               012712-131
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FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: TEEKIN, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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INFORMATION FOR SEQ ID NO: 6:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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MOLECULE TYPE: protein

US-09-948-429B-6
irE: amino acid
TOPOLOGY: linear
i MOLECULE TYPE: protein
US-10-124-905-6
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Sequence 67, Appl.
Sequence 9, Appl.
Sequence 9, Appl.
Sequence 9, Appl.
Sequence 13, Appl.
Sequence 13, Appl.
Sequence 14, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
Sequence 15, Appl.
Sequence 17, Appl.
Sequence 17, Appl.

0.05-09-25-179-67-00-05-00-09-17-410-5-00-09-17-410-5-00-09-17-410-5-00-09-17-410-5-00-09-17-410-5-00-09-17-410-5-00-09-17-410-5-00-09-17-410-68-0-09-17-410-68-0-09-17-410-09-1

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March 29, 2003, 09:14:52 ; Search time 9.16222 Seconds (without alignments) 1531.829 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                US-09-758-173-6
1242
1 MSDPAQLIGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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1: /cgn2 6/prodata/1/pubpaa/USOB NEW FUB.pep:*

2: /cgn2 6/prodata/1/pubpaa/USOB_NEW FUB.pep:*

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14: /cgn2 6/prodata/1/pubpaa/USOB_PUBPCOMB.pep:*
                           GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237916 segs, 58723674 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                  Run on:
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Sequence 2, Appli

ALIGNMENTS

Sequence 118, Sequence 99, Sequence 17,

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESSONDERICE ADDRESS: COMPUTER READABLE FORM:

WREILUM TYPE: Flogpy disk
COMPUTER: Tab C compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: APPLICATION NUMBER: US 08/487,550
FILING DATE: APPLICATION NUMBER: US 08/487,550
FILING DATE: APPLICATION NUMBER: US 08/487,550
FILING DATE: APPLICATION NUMBER: US 08/487,550 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street 012712-131 Sequence 6, Application US/10124905; Patent No. US20020166136A1 GENERAL INFORMATION: RAGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION
TELECHONE: 703-836-6620 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acids 703-836-2021 USA 22314 COUNTRY: STATE: Sequence 8, Applisequence 34, Applisequence 38, Applisequence 52, Applisequence 72, Applisequence 56, Applisequence 10, Applisequence 1, Applisequence 24, Applisequence 65, A

Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 24, Appli Sequence 20, Appl Sequence 50, Appl Sequence 50, Appl

US-10-124-905-6 US-09-948-429B-6 US-09-924-430-8 US-09-992-600A-8 US-09-82-69BA-24 US-09-726-28-42 US-09-909-567B-50 US-09-249-011A-22

11242 11242 1068 1068 997.5 960.5 944.5 946.5 946.5 946.5 946.5 935

US-09-799-514-8 US-09-889-053-34 US-09-889-053-34 US-09-726-258-62 US-09-726-258-51 US-09-726-258-72 US-09-726-258-72

US-09-859-053-30 US-09-995-693-1 US-09-740-002-24 US-10-006-593-69

924.5 909.5 904.5 901.5

Description

SUMMARIES

Query Match Length DB

Score

Result

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The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or its fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of CAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphatemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHrP monoclonal antibody clone protein sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A human monoclonal antibody to parathyroid hormone related protein. - useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone including metastasis, and pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.6%; Score 1063; DB 21; Length 239; 86.2%; Pred. No. 1.9e-58; ive 11; Mismatches 22; Indels 0
/label= Leu, Pro, His, Arg
                                                                        /label= Phe, Ser, Tyr, Cys
                                                                                                                                                 Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31; Page 51-52; 88pp; Japanese.
                                                                                                                                                 /label= Leu, Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0188196.
98JP-0196729.
                                                                                                                                                                                                                                                                                                                                                                           98JP-0304793.
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Best Local Similarity 86.2*
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-286723/25.
N-PSDB; AAA13927.
                                                                                                              Misc-difference 117
                                      Misc-difference 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention
                                                                                                                                                                                                                          JP2000080100-A
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1998;
26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1998;
                                                                                                                                                                                                                                                                                              21-MAR-2000
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121 FTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

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Search completed: March 29, 2003, 09:10:18 Job time : 26.5816 secs

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17-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; parathyroid hormone related protein; PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; STRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                    YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                              85.7%; Score 1065; DB 21; Length 239;
85.8%; Pred. No. 1.5e-58;
iive 15; Mismatches 19; Indels 0;
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                                Claim 31; Page 34-35; 88pp; Japanese.
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including metastasis, and pain
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1 monoclonal antibody to parathyroid hormone related protein. -
for treating hypercalcemia, rheumatoid arthritis, cancer of bone
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86.2%; Pred. No. 1.9e-58;
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98JP-0188196
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included are anti-human Fas antibody CDR peptides (AAB12902-B12907).

Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences

AAA78213-A78266. Primers used for sequencing the human IG DNA used in the invention are represented by sequences AAA78277-A78318 and

AAA783215-A78337, while humanised anti-Fas IG DNA sequencing primers are represented by sequences AAA78217-A78334 and AAA78217-A78324 and AAA78217-A78324 and AAA78217-A78324 and AAA78318-A78324 and are used in the production of the agent of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; parathyroid hormone related protein; PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrcme; SIRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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89.5%; Pred. No. 2.4e-61;
iive 10; Mismatches 15; Indels 0
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98JP-0196729
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Best Local Similarity 89.5'
Matches 214; Conservative
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26-JUN-1998;
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                                             parathyroid hormone related protein (PTHTP). The annoclonal antibody or its fragments, following the etimulation of PTHTP has the following properties: (a) inhibits intracellular elevation of CAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcement, theumatoid arthritis, cancer of bone including metactasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphatemia. It has antiarthritis, cytostatic and antiinflammatory activities. The present sequence represents a human PTHTP monoclonal antibody clone protein sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQTP 120
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                                   present invention describes a human monoclonal antibody to
                                                                                                                                                                                                                                                                                                                                         Length 239;
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                                                                                                                                                                                                                                                                                                                                       87.2%; Score 1083; DB 21;
87.4%; Pred. No. 1.1e-59;
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                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
Claim 31; Page 45-46; 88pp; Japanese.
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98JP-0196729
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                       239 AA;
                                                                                                                                                                                                                                                               present invention
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181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                     Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis; autoimmune disease; rheumatoid arthritis; therapy; human;
                                                                                                                                                                                                                                                                                                          note= "complementarity determining region 1 from CH11 light chain"
                                                                                                                                                                                                                                                                                                                                                     'note= "complementarity determining region 2 from
CH11 light chain"
                                                                                                                                                                                                                                                                                                                                                                                              /note= "complementarity determining region 3 from CH11 light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of anti-Fas protein humanised antibodies - for use in inducing apoptosis on Fas expressing cells in the treatment of autoimmune diseases, especially rheumatoid arthritis
                                                                                                                                Anti-human Fas humanised antibody CH11 light chain VL-KY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haruyama H, Nakahara K, Serizawa N, Takahashi T;
Yonehara S;
                                                                                                                                                                                                                                                   label= Sig_peptide
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/label= Mat_protein
                                                                                                                                                                                                                                 location/Qualifiers
                                                                  AAW71876 standard; Protein; 239 AA
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label= CDR1
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                                                                                                                                                                            antibody engineering.
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                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLOKPGOSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                   1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSKSLVHSNGNTYLHW
                                                                                                                                                                                                                                                                                                                                                                  1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSW
sequences encoding the humanised antibodies are claimed, as are vectors such as pHkappaKY2-58 including the VL-KY nucleotide sequence (see AAV61359), and host cells such as Escherichia coliphkappaKY2-58 (FERM BP-5861).
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                                                                                                                                                                                                                                    Length 239;
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                                                                                                                                                                                                                                    DB 19;
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89.5%; Pred. No. 2.4e-61;
iive 10; Mismatches 15
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                                                                                                                                                                                                                                                                  Best Local Siminarion
Matches 214; Conservative
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                     239 AA;
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                                                                                                                                                                            Seguence
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AAB12913
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AAB12915 standard; Protein; 239 AA.

AAB12915;

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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein closes not include a J segment, has appopted inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive invention exhibit antirheumatic and immunosuppressive cotivity and can be used to treat autoimmune diseases, especially rhuning properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAD12913-B12918 and the corresponding protein sequences (see AAD12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas IG CRH1 (see Corresponding protein sequences (see AAB12913-B12910). Also included are anti-human Fas antibody, CDR peptides (AAB12902-B12907). Primers apecific for the anti-human Fas antibody, Ilght, heavy and kappa chains used in the invention are represented by sequences AAA78210-B12918 and AAA8313-A78317-A78318. And AAA8313-A78317-A78318 and AAA8313-A78317-A78318 and AAA8313-A78317 are appended anti-Fas Ig DNA sequencing primers are represented by sequences AAA78318-A78317. Primer sequences AAA78312-A78312 are appended anti-Fas Ig DNA, and are used in the production of the agent of the invention.
                                        Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human Fas humanizing antibody-containing antirheumatic agents
                                                                                  Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunogaptession; autoimmune disease; treatment; rheumatism; anti-Fas antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 68-69; 109pp; Japanese.
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16-NOV-2000 (first entry)
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Query Match
Best Local Similarity 90.04
Matches 215; Conservative
                                                                                                                239 AA;
                                                                                                                  Sequence
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                                                                                                                                                                                                                                            61 YLQKPQQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVP 120
                                                                                                                                                                                                                                                                                                       PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLMNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                            1 MSLPAQLIGILLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                      181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 SGNGQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                      Query Match 89.6%; Score 1113; DB 21; Length 239; Best Local Similarity 90.0%; Pred. No. 1.6e-61; Matches 215; Conservative 9; Mismatches 15; Indels 0;
239 AA;
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Seguence

g ઠે q ò d ઠે 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9

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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein activity ingredients an immunoglobulin M (IgM) protein. The IgM protein close not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autolimmune diseases, especially. The agents included in the invention has human Pas-antigen creumatism. The IgM molecule used in the invention has human Pas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM is and heavy chains (see AAB12913-B12918 and the cucleotide sequences of the humanised anti-human Fas in GH11 (see AAAP820-A78206) and protein sequences (see AAB12913-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12910). Primers specific for the anti-human Fas antibody, Ilght, heavy and kappa chains used in the invention are represented by sequences by sequences AAA78213-A78366. Primers used for sequences by sequencing primers are represented by sequences AAA78213-A78317, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78313-A78317, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78313-A78367. Primer represented by sequences AAA78318-A78367. Primer represented by sequences AAA78318-A78367. Primer represented by sequences AAA78318-A78367. Primer represented by repres
                                                                                                                                                                                                                                                                                                                               Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #82.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Antirheumatic agent, immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism;
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N-PSDB; AAA78269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-Fas antibody.
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AAB12915
AAB
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                                                                                                                               20-MAR-1998;
                                                                                                                                                            21-MAR-1997;
                                                                                                   23-SEP-1998.
                                                                       EP866131-A2
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 Region
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                                     This is the amino acid sequence of a humanised anti-Fas antibody CC CH11 light chain, deasignated VL-KF. VK-KF is based on the light chain (see AAW71889) of murine anti-human Fas monoclonal antibody CH11. The humanised sequence was designed following selection of donor residues from (TH11 to be grafted onto acceptor molecule RPW16410'CL. 4 Light chain sequences (see AAW71876-19) have been designed, which are can be used in combination with either of 2 heavy chain sequences (see AAW71880-81) to provide novel, claimed humanised CH11 IgM antibodies that lack a J chain. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells capteressing Fas (e.g. synovicoryces) and are useful in the treatment of autoimmune disease and chronic rheumacoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as pikrappakf2-19 including the VL-KF nucleotide sequence (see AAV61360), and host cells such as Bscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YQQKPGQPPKLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVP 120
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autoimmune disease; rheumatoid arthritis; therapy; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "complementarity determining region 1 from
CH11 light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "complementarity determining region 2 from
CH11 light chain"
                                                                                                                                                                                                                                                                                                                   89.6%; Score 1113; DB 19; Length 239; 90.0%; Pred. No. 1.6e-61; tive 9; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-human Fas humanised antibody CH11 light chain VL-RY.
                Claim 23; Page 96-97; 187pp; English.
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Matches 215; Conservative
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                                                                                                                                                                                                                                                                                          239 AA;
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                                                                                                                                                                                                                                                                                            Sequence
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This is the amino acid sequence of a humanised anti-Fee antibody CH11 light chain, designated VL-RY. VL-RY is based on the light chain, designated VL-RY. VL-RY is based on the light chain (see AAM71889) of murine anti-human Fee monoclonal antibody CH11. The humanised sequence was designed following selection of donor residues from CH11 to be grafted onto acceptor molecule RPMIGATO. Lt. 4 Light chain sequences (see AAW71886-79) have been designed, and each can be used in combination with either of 2 humanised CH11 IgM antibodies that lack a J chain. These humanised anti-human Fee entibodies are capable of inducing apoptosis in cells arti-human ferses and are useful in the breatment of autoimmune disease and chronic rheumatoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as plkeappaRY2-10 including the VL-RY nucleotide sequence (see AAW6136), and host cells such as Bscherichia coli
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114...122
/label= COR3
/note= "complementarity determining region 3 from
CH11 light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of anti-Fas protein humanised antibodies - for use inducing apoptosis on Fas expressing cells in the treatment of autoimmune diseases, especially rheumatoid arthritis
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Yonehara S;
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Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #84.
                                                                              61 YLQKPGQSPRLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCSQSTHVP 120
                                                                                                                                                                                                                     61 YQQKPGQPPRILLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                  121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                             181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism; anti-Fas antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB12916 standard; Protein; 239 AA.
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N-PSDB; AAA78270.
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89.9%; Score 1116; DB 21; Length 239; 90.4%; Pred. No. 1e-61;

Query Match Best Local Similarity

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61 YOOKPGOPPRILITYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                121 PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                      1 MRLPAQLIGILMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSKSLVHSNGNTYLHW 60
0; Gaps
                          1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                     181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYENGHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                               Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis; autoimmune disease; rheumatoid arthritis; therapy; human; antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 1 from CH11 light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of anti-Fas protein humanised antibodies - for use in inducting apoptosis on Fas expressing cells in the treatment of autoimmune diseases, especially rheumatoid architits
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8; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
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                                                                                                                                                                                                                                                                               AAW71877 standard; Protein; 239 AA.
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label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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Yonehara S;
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(SANY ) SANKYO CO LTD.
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                                                                       Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YOOKPGOPPALLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PTFGGGTKVEIKRTVAAPSVPIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSLPAQLIGILLICVPGSSGEVVWTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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                                                                                                                                                                                                                                                                                                                                          Example 8; Fig 4a; 89pp; English.
                                                                                                                                                          Anderson DR, Hanna N, Brams P;
                                                    22-MAY-2001; 2001WO-US16364.
                                                                                     22-MAY-2000; 2000US-0576424.
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                                                                                                                       (IDEC-) IDEC PHARM CORP.
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                29-NOV-2001.
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This is the amino acid sequence of a humanised anti-Fas antibody CC CH11 light chain, designated VL-RF. VL-RF is based on the light chain (see baw11889) of mutine anti-human Fas amonoclonal antibody CC CH11. The humanised sequence was designed following selection of Gonor residues from CH11 to be grafted onto acceptor molecule RPMISIG10. L 4 Light chain sequences (see AAW11816-79) have been designed, and each can be used in combination with either of 2 heavy chain sequences (see AAW1880-81) to provide novel, claimed humanised antibodies that lack a J chain. These humanised antibodies are capable of inducing apoptosis in cells expressing Pss (e.g. symoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as phtkappaRP2-52 including the VL-RF nucleotide sequence (see AAV61362), and host cells such as Bscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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/label= CDR2
/note= "complementarity determining region 2 from
CH11 light chain"
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89.9%; Score 1116; DB 19; Length 239;
Best Local Similarity 90.4%; Pred. No. 1e-61;
Matches 216; Conservative 8; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haruyama H, Nakahara K, Serizawa N, Takahashi T;
Yonehara S;
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                                                                                                                                                                                                                                                                                                                                                                   1..239
label= Mat_protein
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= CDR1
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                                                                                                                          2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy variable genes (see also AAT62511 and AAT13847) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01817-19 and AAW01821-22). The primatised antibodies have also been produced (see also AAW01817-19 and antipodies have also been produced (see also AAW01817-19 and awking them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1242; DB 18; Length 239; 100.0%; Pred. No. 1.7e-69; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaque primatized 7B6 light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW63762 standard; Protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DR, Brams P, Hanna N;
                                                                                           Claim 8; Fig 9A; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0746361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US19906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-286£01/25.
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                               239 AA;
N-PSDB; AAT62511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9819706-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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ID AAW
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This sequence represents a primatized form of the antibody 786 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MADs s) that bind selectively to BT.1 (CD80) or to BT.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such MADs are specific immunosuppressants for treatment of diseases involving a call opathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiapates mellitus, rhemmatory disease and tumours operation and inflammatory disease and tumours (obtionally the chort diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours to Optionally combined with other proteins or small molecule immunosuppressants. Blocking BT/CD28 interactions or induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, macaque monkey, light chain, primatised antibody, 7B6 antibody, neuroprotective, apoptosis inducer, allergy, CD28 receptor antagonist, by 1 antigen, CD80, B7 2 antigen, CD86, B cell cancer, metastasis, tumour, B cell ymphoma; B cell leukaemia, autoimmune disease, graft-vs-host disease, immunosuppression, organ rejection, interleukin-2; IL-2; mutant, mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequence of primatised form of the light chain of 7B6 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PTFGGGTKVBIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YOOKPGOPPALLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGOGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLPAQLIGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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                                                                                 New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1242; DB 19; Length 239; Best Local Similarity 100.0%; Pred. No. 1.7e-69; Aatches 239; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU11540 standard; Protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                           Example 7; Fig 4a; 87pp; English.
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Chimeric - Macaca sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AA;
N-PSDB; AAV35486.
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Human PTHYP monocl Human PTHYP monocl Human PTHYP monocl 3F4 Human 1964 exp Murine anti-Porcin Human PTHYP monocl

Monoclonal antibod Protein #1 in inve Human PTHrP monocl Human PTHrP monocl Humanised monoclon

Humanised 323/A3

Perfect score: Scoring table:

Run on:

Seguence:

Database

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Monoclonal antibody; cynomolgus monkey; macaque; 786;
primatised antibody; 87 antigen; CDS9; immunosuppressive;
autoimmun disease; idiopathic thrombocycopaenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
type 1 diabetes mellitus; graft versus host disease;
hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                     Primatised anti-human B7.1 antigen antibody 7B6 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shestowsky WS;
                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                            4896
                                                                                                                                                                                                                    AAW90927
                                                                                                                                                                                  AAE12714
                                                                                                                                                                                                                                                                                                                                                                  AAW01819 standard; Protein; 239 AA.
                                                                                                                                                                                                                            ABB74
ABB74
                                                                                                                                               AB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US10053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
(IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-108638/10.
25-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9640878-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996.
 1110
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 Macaque primatized Protein sequence o Anti-human Fas hum Anti-human Fas hum Anti-human Fas hum Anti-human Fas imm Anti-human Fas simm
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Fas hum
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                                                         March 29, 2003, 09:06:23 ; Search time 24:5816 Seconds (without alignments) 1295:559 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                              A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                                                                                                            1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
       GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      908470 seqs, 133250620 residues
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                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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AAW63762
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AAW71877
AAW71878
AAB12914
AAB12915
AAW71876
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AAW71879
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Maximum DB seq length: 200000000
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1242
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Match I
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Chimeric 6G4.2.5 I Murine variable re Chimeric anti IL-8 Chimeric monoclona Anti-IL-8 mouse-hu Chimeric Mb 6G4.2 Chimeric anti IL-8

Humanised anti-Fas HFE7A de

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G--VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 236
Hypothetical 24.9 kDa protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
4-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6-JUN-2002 (TrEMBLrel. 20, Last annotation update)
6-JUN-2002 (TrEMBLre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
35.2%; Score 437.5; DB 4; Length 237;
Best Local Similarity 42.4%; Pred. No. 3.6e-33;
Matches 101; Conservative 44; Mismatches 80; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSEQUENCE FROM N.A.
TISSUE-TONSIL;
A Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
L Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R BMBL; BCOG0233, AAH20233.1; -.
R BML; BCOG0339; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R SWART; SM00409; IG; 2.
SWART; SM00409; IG; 2.
SWART; SM00409; IG; 1.
R SWART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                 A Straubberg R.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

R RBL; BC022098; AAH22098.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R Pfam; PP00047; Ig. 2.

SWART; SW00409; IG; 2.

SWART; SW00409; IG; 2.

R SWART; SW00409; IG; 1.

R SWART; SW00409; IG; 1.

R PROSITE; PS00290; IG MHC; UNKNOWN_1.

R PROSITE; PS00290; IG MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                TISSUE=TONSIL;
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QBWUK4;
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Search completed: March 29, 2003, 09:14:38 Job time : 22.6765 secs

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Matches 103; Conservative
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                      PRELIMINARY;
          Pfam; PF00047; ig; i. SMART; SM00406; IGv; i. NON_TER 1 1 1 1 NON_TER 114 114
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=PRIMARY B-CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                           SEQUENCE
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Q8WTU6
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                                                                                                                   wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (Secry).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF152371; AAD40242.1; -...

R HSSP; PO1679; 2FBJ.

R InterPro; IPR001560; Ig_NHC.

R InterPro; IPR001560; Ig_W.

R FART; SM00406; IG_V.

R SWART; SM00410; IG_like; 1.

R RAART; SM00410; IG_like; 1.

R PROSITE; PS00290; IG_MHC, UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVEIKRTVAAPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 DGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIKRADAAPTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 FIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 SIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWIDQDSKDSTYSM 175
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         21 EVVMTOSPLSLPITPGEPASISCRSSOSLKHSNGDTFLSWYQOKPGOPPRLLIYKVSNRD 80
 01-MAÝ-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.9%; Pred. No. 3.7e-52;
Matches 118; Conservative 42; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 SSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035034; AAD56270.1; -.
HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AA
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                                                                                                                SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 OKPGOPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVBABDVGVYFC--GQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 VKAG--VETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTE 231
                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLPLLTLCT-GSEASYELTOPP-SVSVSPGQTARITC-----SGDALPKQYAYWYO 55
                                                                                                                                                                                 21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                    Query Match 37.2%; Score 462.5; DB 4; Length 114; Best Local Similarity 78.9%; Pred. No. 5.7e-36; Matches 90; Conservative 12; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022823; AAH22823.1; -. Hypothetical protein. SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
114 114
114 AA; 12775 MW; 070531E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24, 9 kba protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.1%; Score 460.5; DB 4
42.7%; Pred. No. 2.4e-35;
tive 45; Mismatches 70
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Gaps

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60 PGEPPKLLISEGNTLRPGVPSRFSSSGYGTDFVFTIENTLSEDVADYYCLQSDNMPLTFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 GCTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFGGGTKVF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 LLIXYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE 190
                                                                                                                                                                                                                                                                                                                                   65 PGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPPTFG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 IKRADAAPIVSIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERONGVLNSWID 184
                                                                                                                                                                                                                                       5 APLLSLLLCVSDSRAETTVTQSPASLSVATGEKVTIRCITSTDI-----DDDMNWYQQK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGIAN-----YLNWYQQKPDGTVK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERONGV
                                                                                                                                                                                             5 AQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                           Query Match 52.9%; Score 656.5; DB 11; Length 234; Best Local Similarity 54.5%; Pred. No. 8.4e-54; Matches 128; Conservative 30; Mismatches 72; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.8%; Score 655.5; DB 11; Length 233; Best Local Similarity 55.5%; Pred. No. 1e-53; Matches 127; Conservative 34; Mismatches 63; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 INSWIDQDSKDSTYSMSSTLILIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databages.
EMBL, BC013496; AAH13496.1; -.
InterPro; IFR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hyporterical protein_1
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25702 MW; 148377F9C1CD0AEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypochetical 25.8 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=COLON;
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SEQUENCE
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Q9R1A5;
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Q9R1A5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 NPPTFGVGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                    176 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSLPAQLLGLLL--CVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                 181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.7%; Score 667; DB 11; Length 235; 53.1%; Pred. No. 8.7e-55; ive 37; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643; AAH06643.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028540; AAH28540.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAM; PF00047; 1g; 2. PROSITE; PS00290; IG MHC; UNKNOWN 1. SEQUENCE 235 AA; Z6021 MW; SFC73BDEBDSEBFEF CRC64;
                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown (protein for MGC:6582).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 53.18
Matches 128; Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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TISSUR=MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] =
SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia, Eutheria
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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Q8R028

RESULT 9
08R028
1D 08R02
AC 08R0
DT 01-JI
RRP 82R0
RRP 82R0
RRA 82

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116 FTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                           PEGM; PF00047; 19; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=COLON;
                                                            SEQUENCE FROM N.A.
                  NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R062
Q8R062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 FIFEGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175
  61 YLQKPGQSPQLLIXLVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLP 120
                                                                                    121 YTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                              121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSVPTQVLGLLLCLTGARCDIQLTQSPASLSASVGETVTITCRASENIY----SYLAW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                               181 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                           181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25-9 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 691.5; DB 11; Length 234; 54.0%; Pred. No. 4.2e-57; tive 44; Mismatches 61; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC019474; AAH19474.1; -.
R InterPro; IPR003599; 19_-.
R InterPro; IPR003599; 19_-c1.
R InterPro; IPR003599; 19_-c1.
R InterPro; IPR003599; 19_-v.
R Pfam; PPC0047; 19; 2.
SMART; SM00409; 1G; 2.
SMART; SM00409; 1G; 1.
R SMART; SM00409; 1G; 1.
R SMART; SM00409; 1G; 1.
R PROSITE; PS00290; 1G MHC; UNKNOWN_1.
R PROSITE; PS00290; 1G MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                              080CP0;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse) h.r.dara: Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AA
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 54.09
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1)
SEQUENCE FROM N.A.
TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Q91WF8;
                                                                                                                                                                                                                                                                              Q8VCP0
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091WF8
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ID Q
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56 YQQKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYXCQQYSQFP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YOOKPGOPPRILIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGOGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISN----YLNW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSLPAQLIGILILICVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISN----YLNW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                    Query Match 55.0%; Score 682.5; DB 11; Length 234; Best Local Similarity 55.2%; Pred. No. 3e-56; Antoches 132; Conservative 35; Mismatches 67; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292, AAH15292.1; -.
InterPro; IPR003006; Ig MHC.
InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                           Hypothetical protein.
SEOUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25,9 kba protein.
Mus musculus (Mouse)
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Gaps

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60 YLQKPQQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 YTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 QNGVLNSWTDQDSKDSTYSMSSTLTLTKYDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLPAQLIGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.1%; Score 808; DB 11; Length 23 Best Local Similarity 64.4%; Pred. No. 4.7e-68; Matches 154; Conservative 32; Mismatches 53; Indels
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003556; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG like; 1.
                                                                                                                                                                                                                                                                                                                                                                      67.9%; Score 843.5; DB 11; Length
66.5%; Pred. No. 2.1e-71;
tive 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VC55 PRELIMINARY; PRT; 239 AA.
Q8VC55;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.5%
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
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     181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                   QBVCI6;
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
Hypothetical 26.2 kDa protein.
Bukaryota; Mcraca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, BC019760, AAH19760.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-W.
Pfam; PF00047; ig; 2.
SWART; SM00409; IG; 2.
SWART; SM00406; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 864.5; DB 11; Length 68.2%; Pred. No. 2.2e-73; tive 30; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitded (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO2035; AAN02035.1; -.
HSSP; PO16/79, ZPBJ.
InterPro; IPR003599; Ig.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kba protein.
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                                                                                RESULT 2
QBVCI6
AC QBVCI6;
DT 01-MAR.;
DT 01-JMAR.;
DT 01-JMAR.;
DE Hypothed
OC Bukaryol
OC Mammalia
OC Mammalia
OC TISSUE
RR SEQUENCI
RA SETAUBB
RI SUDMITTA
DR SUDMITTA
DR INTERPRI
DR INTERPRI
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DR INTERPRI
DR SMART;
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Gaps 9 Q96661 homo sapien Q99m11 mus musculu Q96669 homo sapien Q9178 homo sapien Q9185 homo sapien Q9185 homo sapien Q9186 homo sapien Q9186 homo sapien Q91181 homo sapien Q91179 homo sapien Q9177 mus musculu Q92589 mus musculu Q92589 mus musculu Q9110 mus musculu Q9110 mus musculu Q91178 mus musculu

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61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
88.8%; Score 1103; DB 4; Length 239;
Best Local Similarity 88.7%; Pred. No. 7.6e-96;
Matches 212; Conservative 15; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2002) 4412362.1; -. Hypothetical protein. SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 26.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA
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            099M11
086L69
090L169
090L85
090L85
090L86
090L86
090L79
080L79
080D0
090L70
090L70
090L70
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Q925S9
Q96PF6
Q920E6
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Q9JL78
Q9NOW5
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Q9JL84
Q921A6
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TISSUE=LUNG;
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MEDLINE=8222190; PubMed=6283537;
MEDLINE=8222190; PubMed=6283537;
MINCLEDCTIGE sequences of gene segments encoding membrane domains of munoclobulin gamma chains.";
Immunoglobulin gamma chains.
Immunoglobulin ga
PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 442
                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                   VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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                                            4 ;
    Length 399;
; Score 1117; DB 1; Length 36; Pred. No. 4e-72; 43; Mismatches 74; Indels
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  43.6%;
Query Match
Best Local Similarity 63.49
Matches 210; Conservative
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                                   MEDLINE-74175517; PubMed-4831970; Bourgois A., Fougereau M., Rocca-Serra J.; Bourgois A., Fougereau M., Rocca-Serra J.; Bourgois A., Fougereau M., Rocca-Serra J.; Experimention of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
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                                                                                                                                                 de Preval C., Fougereau M.; betermination of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
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       Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF60047; ig; 2. SMART; SW00410; IG like; 1. SMART; SW00410; IG like; 1. SMO3407; SG01207; IGC1; 2. ISSO17E; PS002507; IG MHC; 1. Immunoglobulin domain; Immunoglobulin C region.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR03500; Ig_like.
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                               MYELOMA PROTEIN MOPC 173
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dognin M.J., Lauwereys M., Strooberg A.D.;

"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotypic forms.";

Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

P. M.SCELLANGOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-82037861, PubMed-6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the
IgGaa and IgGab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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Best Local Similarity 61.3%; Pred. No. 2.1e-72;
Matches 206; Conservative 52; Mismatches 71; Indels 7;
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Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
                                                                                                                                                                                                         335 AA
299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00479; -; NOT_ANNOTATED_CDS.
PIR; A02153; GZMSAB.
HSSP; P01842; 7FAB.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_like.
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MEDLINE=82037777; Pubmed=6794027;
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SMART; SM00410; IG like; 1.
SMART; SM00407; IGC1; 2.
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GCAA MOUSE
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                                                                                       267 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 326
                                                                                                                        172
                                                                                                                                                                    61 -LYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114
1 AKTTPPSVYPLAPGSAAQINSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                         115 --SSVPIPPPKPXDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                                                                                                                                                                                               233 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                             209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL
                                                                                                                                                327 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSR
                                                                                                                                                                                                             387 DELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85027161; PubMed=6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
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01-MG-1991 (Rel. 19, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 gamma-3 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                         447 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
                                                                                                                                                                                                                                                                                         segment.";
Nucleic Acids Res, 11:6775-6785(1983).
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EMBL; V01526; CAA24767.1; ALT_SEQ.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003609; Ig_like.
Pfam; PP00047; ig; 3.
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SMART; SM00407; IGC1; 2.
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MEDLINE=81198976; Pubmed=6262729; Yamawaki-Kataoka Y., Miyata T., Honjo T.; Yamawaki-Kataoka Y., Miyata T., Honjo T.; "The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain gere; further evidence for intervening sequence-mediated domain transfer."; Nucleic Acids Res. 9:1365-1381(1981).
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                                                                                                                                                                                                                                                                                         150 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 209
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                                                                                                                                                                                                         44.0%; Score 1126; DB 1; Length 398; 63.8%; Pred. No. 9.1e-73; ive 46; Mismatches 69; Indels
                                                                                                             E -> G (IN REF. 2).
E -> O (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
                                                                                            (POTENTIAL)
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-2A chain C region, A allele.
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149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDINE=80045036; PubMed=115593;
MEDINE=80045036; PubMed=115593;
Horjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
"Cloning and complete nucleotide sequence of mouse immunoglobulin call 18:559-568(1979).
                                          EMBL, J00451; -; NOT_ANNOTATED_CDS.

PTR; B02156; G3MSC.

HASSP, P01857; IFC1.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003507; Ig_c1.

InterPro; IPR0047; Ig_lake.

Pfam; PF0047; Ig_lake; I.

SMART; SM00410; IG_like; I.

SMART; SM00407; IGGl; 2.

PROSITE; PS00290; IG_MHC; I.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

Transmembrane; Alternative splicing.
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                                                                                                                                                                                                                                                                      44.4%; Score 1137; DB 1; Length 329; 64.0%; Pred. No. 1.2e-73; ive 46; Mismatches 69; Indels 4
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329 AA; 36228 MW; F45827174182BAD6 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
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HINGE.
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Matches 212; Conservative
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44.2%; Score 1133; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 2.9e-73;
Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps
SEQUENCE OF 323-393 FROM N.A.
MEDLINE=82197626; PubMed=6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                      SEQUENCE OF 323-366 FROM N.A.
MEDIATE-8115285; PubMed=6799207;
MROGETS J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domaiñ; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
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MGD; MGI:96446; 1Gh-4.
InterPro; 1PR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF00047; ig; 3.
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393 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE=80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                             MEDLINE=80045036; PubMed=115593; Monjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
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"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126.837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:95446; Igh-4.
InterPro; IPR003006; Igh-HC.
InterPro; IPR003597; Ig_cl.
EnterPro; PR0047; ig_l.
SWART; PR00407; IGcl.
PROSITE; PS00290; IGHHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                  (Rel. 01, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain.";
Nucleic Acids Res. 6:3305-3321(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE=78242288; PubMed=98524;
                                       PRT;
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J. Biol. Chem. 253:6068-6075(1978)
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MEDLINE=73008889; PubMed=5073237;
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00795; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
PIR; A02159; GIMS.
                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                           Ig gamma-1 chain C region.
Mus musculus (Mouse).
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GlycoSuiteDB; P01868; -.
                                       STANDARD;
                                                                                                                                                                                                                                                                        gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10090;
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                                    GC1_MOUSE
P01868;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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62.0%; Pred. No. 9.9e-74;
tive 55; Mismatches 61; Indels 1
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N -> D (IN REF. 3).
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region, secreted form.
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GLYTLISSUTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG--GDCKPC----ICTG 113
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%; Score 1148; DB 1; Length 326;
63.1%; Pred. No. 2e-74;
iive 52; Mismatches 61; Indels 10;
                                                                          478
                                                                                       GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                             GC1 RAT STANDARD; PRT; 326 AA. P20759; 01-FEB-1991 (Rel. 17, Created) 15-JUL-1999 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 gamma-1 chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89232738; PubMed=3149946;
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Rattus morvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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44.6%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 4.9e-74;
Matches 214; Conservative 44; Mismatches 69; Indels 9;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region.
                                                                                                                                                                                                                                                                                                                           333 AA
                                               294 EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326
446 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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333 AA;
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PRE 2.

-I-RISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.
-I-MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAWMA-3 HEAVY CHAINS.
-I-MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM OR MOTHER GAWMA-GHAIN SUBCLASS.
-I-MISCELLANEOUS: THE HINGE REGION IN GAWMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE JENSTICKLISSENDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                            176 QYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
                                                                    RDELTKNOVSLICLVKGFYPSDIAVEWESNGOP -- ENNYKTIPPVLDSDGSFFLYSKLTV 443
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-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
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SEQUENCE (DISEASE PROTEIN WIS).
SEQUENCE (DISEASE PROTEIN WIS).
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77118561, PubMed=402363,
Michaelsen T.E., Frangione B., Franklin E.C.;
"Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=77021516; PubMed=823945;
MEDLINE=77021516; PubMed=823945;
Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
"The amino acid sequence of 'heavy chain disease' protein ZUC.
Structure of the Fc fragment of immunoglobulin G3.";
Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
19 gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                                                                                                                                                                                                                           290 AA
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P01860;
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GG3 HUMAN

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5 the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 253 KTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 312 124 313 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 372 184 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat. Gaps 64 DIMER).
DIMER).
DIMER).
DIMER). 65 TPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDG 125 VQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTKG DIMER). -----DKKAEPKSCD 8 TVSSELKTP---LGDTTHTCPRCPEPKSCDTPPCPRCPEPKSCDTPPPCPRCPEPKSCD DIMER). DIMER) 22; INTERCHAIN (WITH HEAVY CHAIN DI Length 290; Indels REMOVED POST-TRANSLATIONALLY PYRROLIDONE CARBOXYLIC ACID E69CBC95705B2F46 CRC64; 3.9e-75; ches 26; S -> N (IN OMM).
/PTIG=VAR 001 DB 1; (GLCNAC. -> EB (IN ZUC) FTIG=VAR 003891 003895. 003896 L (IN OMM) A (IN OMM) $F -> Y (I\overline{N} OMM)$ /FTIG=VAR 00389 ; Score 1157; Di ; Pred. No. 3.9e 20; Mismatches 212 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV-----P -> L (IN/ /FTId=VAR FTIG=VAR FTId=VAR FTIG=VAR N-LINKED HINGE. CH2. CH3. EMBL, J00231, AAA52805.1; ALT_SEQ. PIR, A02149; GHUWI. PIR, PO1857, IFC1. Genew, HGNC:5527; IGHG3. MIM; 147120; InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfan; PF00047; Ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PR0SITE; PS00290; IG_MHC; 1. 290 AA; 32331 MW; 45.2%; 76.2%; Best_Local Similarity 76.2 Matches 218; Conservative 73 183 289 43 58 73 766534483374767 227 279 139 182 227 227 DOMAIN BEPEAT REPEAT REPEAT REPEAT MOD RES CARBOHYD DISULFID DISULFID DISULFID DISULFID DISULFID CARBOHYD DISULFID DISULFID DISULFID SEQUENCE DISULFID Query Match DISULFID DISULFID DISULFID MOD RES VARIANT VARIANT /ARIANT VARIANT VARIANT VARIANT VARIANT DOMAIN ò 유 ò ద ò 셤

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Biochemistry 10:26-31(1971).
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Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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the carboxyl-terminal
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                                                                                                                                                                                                                                  MEDIINE=75036072; Pubmed=4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig 1gG2
                                                                                                                                                                                                                                                                                                                                                  MEDINE=75036073; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
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"Structure of heavy chain from strain 13 guinea pig
fimunoglobulin-(5(2). 3. Amino acid sequence of the region around
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
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DISULFID 28 79 INTERCHAIN (WITH A LIGHT CHAIN).

DISULFID 105 105 INTERCHAIN (WITH A LIGHT CHAIN).
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202 N-LINKED (GLCNAC. . .).
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4) 36074 MW, 5D231B7164D1FBA9 CRC64;
                                                                                                                 Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea jimmunoglobulin-G(2). II. Amino acid sequence of inmunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                    SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                     lochemistry 13:4796-4803(1974)
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HSSP, P01842; 7FAB.
Interpro; 1PR003006; Ig_MHC.
Interpro; 1PR003597; Ig_C1.
Interpro; 1PR003600; Ig_like.
Pfam; PF00047; Ig; 2.
SWART; SMO0410; IG_like; 1.
SWART; SMO0410; IG_like; 1.
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Best Local Similarity 70.1%
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLSSVVSVTSSS---QPVTCNVAHPAINTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                      47.9%; Score 1226.5; DB 1; Length 323; 69.7%; Pred. No. 5.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Indels
                                                                                                                ( IN ELS. 2).

( IN REF. 2).

( IN REF. 2).

( IN REF. 3 AND 4).

( IN REF. 5).

( IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                     35404 MW; 69E8AA118D579A8B CRC64;
                                                                                                       D11 MARKER).
                                                                   Immunoglobulin domain; Immunoglobulin C region.
NON TER 1 1 1 T -> M (IN D11 MAR)
VARIANT 104 104 T -> M (IN D11 MAR)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1975) to the PIR data bank
                                                                                                     NVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 DVFTCSVMHEALHNHYTQKSISRSPGK 323
                                                                                                                     Pfam, PF00047, ig, 2.
SMART, SM0407, IGc1, 2.
PROSITE, PS00290, IG MHC, 1.
   InterPro, IPR003597, Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     323 AA;
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SEQUENCE OF 4-68.
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P01862;
                                                                                                                   VARIANT
CONFLICT
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SEQUENCE OF 1-128.
MEDLINE=56135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITNE=84030930; PubMed=6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                            LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
                                                                                           38 MIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFLYSRLTVDKSRW 297
      178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
Martens C.L., Moore E.W., Steinmetz M., Hood L., Knight K.L.;
Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gamma globulins, Nobel symp. 3, pp.109-127, Almgvist and Wiksell, Stockholm (1967).
-!- MISCELLANBOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-70110015; PubMed=5461106; Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.; "Sequence studies of the Fd section of the heavy chain of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Pellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                323 AA
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                                                                                                                                                                             QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                               QEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenetics 18:387-397(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin G.";
Biochem. J. 116:249-259(1970)
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                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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HSSP; P01857; 1FC
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15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.; "Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain."; Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
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                                                                                                                Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   MEDLINE-83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH A LIGHT CHAIN)
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35940 MW; 3EDBD811EF208E7A CRC64;
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      40, Last annotation update)
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HINGE.
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MEDLINE=70207560; PubMed=4192699;
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                             Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                        Ig gamma-4 chain C region.
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Genew; HGNC:5528; IGHG4.
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327 AA;
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                                                                                                                                                                          NCBI_TaxID=9606;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AT OR NEAR THE COMPLEMENT-BINDING SITE.
326 REMOVED POST-TRANSLATIONALLY (PROBABLE)
60 S -> A (IN WYELCMA PROTEINS TIL & ZIE).

/FIId=ARR 003889
109 C -> S (IN REF. 3).
35884 MW, 8310878C6878CF9C CRC64;
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CHAIN).
CHAIN).
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INTERCHAIN (WITH A LIGHT CHAIN)
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(Rel. 01, Last sequence update)
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InterPro; IPR001306; IG MHC.
InterPro; IPR001359; IG_C1.
InterPro; IPR001560; IG_16.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_1ike; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00299; IG_MHC; 2.
                                                                               EMBL, J00230; AAB59393.1;
PIR; A02148; G2HU.
HSSP; P01857; 1FC1.
Genew; HONC:5526; IGHG2.
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Matches 300; Conservative
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P01861;
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AC P0186:
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                                                                                                                                                                                                                                                                                    TISSUE=Fetal liver;
MEDLINE=84235992; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
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Cell 29:671-679(1982).
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                                                                  Ellison J.W., Hood L.E.; "Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJINE=80114419; PLANE HORMED HORMED HORMED T., Parr D.M.; Hofmann T., Parr D.M.; Parr D.M.; A note of the amino acid sequence of residues 381-391 of human immunoglobuling gamma chains."; Mol. Immunol. 16:923-925(1979).
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"The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
                                                                                                  heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-69064124; PubMed=5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                       SEQUENCE OF 99-177 AND 310-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
MEDLINE=81007873; PubMed=6774012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                           TISSUE-Fetal liver;
MEDLINE-83001943; PubMed-6811139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
                                     SEQUENCE OF 2-326 FROM N.A. MEDLINE=82197621; Pubmed=6804948;
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                                                                                                                                               SEQUENCE OF 88-115 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 238-275 (ZIE)
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      NCBI TaxID=9606;
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Gaps

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PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequ
16-OCT-2001 (Rel. 40, Last anno
Ig gamma-2 chain C region.
IGHG2.
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P01859;
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GC2 HUMAN

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                                                                                                                                                                     Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of annoclonal Wile of antibody structure. The primary structure of a monoclonal 1931 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L. and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; ig, 3.
SWART; SW00410; IG_like; 1.
SWART; SW00407; IG_like; 2.
FROSITE; PS00290; IG MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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REMOVED POST-TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FTIG=VAR 00388.

D -> E (IN GIM(NON-1) MARKER).

FTIG=VAR 003887.

L -> M (IN GIM(NON-1) MARKER).

/FTIG=VAR_003887.
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INTERCHAIN (WITH HEAVY CHAIN)
INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed-7236608;
Deisenhofer J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00228; AAC82527.1; ALT_INIT
                                                MEDLINE=77070267; Pubmed=1002129;
            Biochemistry 9:3188-3196(1970)
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PDB; 1FC2; 15-JUL-92.
Genew; HGNC:5525; IGHG1.
MIM; 147100; -
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P01857 homo sapien
P01859 homo sapien
P01861 homo sapien
P01870 oryctolagus
P01862 carta porce
P01860 homo sapien
P20759 rattus norv
P20761 rattus norv
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suncus muri
                                                                                                                                                                                                                      March 29, 2003, 09:06:23 ; Search time 11.3969 Seconds (without alignments) 1739.566 Million cell updates/sec
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2561
1 MGWSLILLFLVAVATRVQCE.......MHEALHNHYTQKSLSLSPGK 478
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Search completed: March 29, 2003, 09:16:19 Job time : 22.453 secs
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J. Immunol. 153, 3552-3573, 1994
A;Title: Five purative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma 2a chain constant region - pig (fragment)
C,Species: Sus scrofa domestica (domestic pig)
C,Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                292 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 351
                                                                                                                             352 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 411
                                                                                                                                                          349 CKVNNKDLPAPIERTISKIKGIVRAPQVYILSPPPEQLSRKDVSLTCLAVGFSPEDISVE 408
                                                                                                                                                                                                     412 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 471
                                                                                                                                                                                                                          149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP---G 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 PSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 LTKNOVSLICLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: U03779; NID: 9433123; PIDN: AAA52217.1; PID: 9433124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match

49.2%; Score 1259; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 18e-67;
Matches 230; Conservative 43; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfemily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 RWOOGNVFSCSVMHEALHNHYTOKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 gamma-1 chain C region - synthetic
C; Species: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                           472 LSLSPGK 478
                                                                                                                                                                                                                                                                                                          469 ISRSPCK 475
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A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-20a-1995
R;Filpula, D.
Submitted to the EMBL Data Library, February 1993
A;Description: Screalag method for protein-protein interactions of cloned gene products.
A;Reference number: $31866
A;Accession: $21866
A;Accessi
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Iggamma-2b chain precursor - mouse
C;Species in we mueculus (bouse mouse)
C;Date: 30-Sep-1899 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: 501321
R;de Waele, P.; Pers, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed ac, A;Reference number: 501321, MUID:88329081; PMID:3138116
A;Accession: 501321
A;Molecule type: mRNA
A;Residues: 1-475 cbEl>
A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A;Residues: 1-475 cbEl>
A;Cross-references: EMBL:X13188; NID:951780; munnoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C resion; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
F;20-475/Product: Ig gamma-2b chain #status predicted <AMT>
F;20-475/Product: Ig gamma-2b chain #status predicted <AMT>
F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GQGLEWIGYI--NPNKDGTKFNEKPKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARD 118
                                                                              121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                                                                                                                                                        119 YDY-----DWFAYWGQGTLVTVSAAKTTPPSVYPLAFGCGDTTGSSVTSGCLVKGY 169
                                                                                                                                                                                                                                                                                                                                                                               241 KVDKKAEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV 293
                                                                                                                                                                                                                                                                                                                                                                                                                            230 TVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 VVDVSHEDPBVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 SNGHTEENYKDTABVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTIS 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YISHCRGGVCYGGY--FEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 -----AGPROVGLLPFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEWIWIFLFILSGTAGVQSQVQLQQSGABLARPGASVKLSCKASGYTLTSYGISWVKQRT 60
                                                                                                                                                                                                                              181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                                                                                                        Ouery Match 52.3%; Score 1338.5; DB 2; Length 475; Best Local Similarity 53.8%; Pred. No. 5.5e-72; Matches 262; Conservative 73; Mismatches 131; Indels 21;
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A; Residues: 138-161, L', 163-189, 'FP', 193-474 «YAM»
A; Residues: 138-161, L', 163-1090461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A; Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A; Reference number: A26235; MUID:80081501; PMID:117548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constitute:

An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as 180, the subunits associate into la cicomplex: An immunoglobulin heterotetramer subunit disulfide bonds: In some cases, such immunoglobulin homology cicomplex immunoglobulin c region; immunoglobulin homology cicomplex: Internative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cimi>F157-222/Domain: immunoglobulin homology cimi>F158-250/Domain: immunoglobulin homology cimi>F188-450/Domain: immunoglobulin homology cimi>F188-450/Domain: immunoglobulin homology cimi>F186-220,288-348,394-452/Disulfide bonds: interchain (to light chain) #status predicted
F186-220,288-348,394-452/Disulfide bonds: interchain (to lowayy chain) #status predicted
F186-220,288-348,394-452/Disulfide bonds: interchain (to lowayy chain) #status predicted
F186-220,288-348,394-364/Disulfide bonds: interchain (to lowayy chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Redidues: 138-172, P., 174-189, FP', 193-376, T', 378-474 <TUZ>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6803173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: DNA
A;Residues: 133-161, L.,163-189, FP',193-300, R',302-331, A',333-437, DI',440-474 <OLL>
A;Residues: 133-161, L',163-189, PP',193-300, R',302-331, A',333-437, DI',440-474 <OLL>
B;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
B;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
B;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, R.; Irimura, T.; Takahash
A;Hille: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS.
A;Residues: 1-474 <FIS.
A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
B;Yamawaki-Kateoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Ttle: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from A;Reference number: A02157; MUID:80120716; PMID:6766534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 138-172, 'P',174-189,'FP',193-376,'T',378-474 <TUI>
A;Note: Lye-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, R.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%; Score 1392; DB 1; Length 474; 54.6%; Pred. No. 3.8e-75; ive 73; Mismatches 129; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 234-251 «KIM»
C;Comment: The a allele sequence is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                A; Contents: a allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A26233
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21; Gaps

239 NTKVDKKAEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 291

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C.; Bit

Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber,

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Query Match
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G2MS11
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                                                                        RESULT 10
S6933
Iq heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: S69339; S72664
R; Khamlichi, A.A.; Aucouturier, P.; Freud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: S69339; MUID:95262687; PMID:7744049
A; Residues: 1-374 «KHA>
A; Cross-references: EMBL:X81695
R; Khamlichi, A.A.
Submitted to the EMBL Data Library, September 1994
A; Reference number: S72664
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-140, C'. 142-374 «KH2>
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $40295
19 gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVIJTVLHQDWLNGKEYKCKVSNKALDAPI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNTKVD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 RGGVCYG-GY-FEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDH--YMYWFRQAPGKGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKTISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.3%; Score 1415; DB 2; 60.2%; Pred. No. 1.3e-76; tive 25; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 ----YGOGYRFHSWGOGTLVTVSS-----YGOGYRFHSWGOGTLVTVSS
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Matches 286; Conservative
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476
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submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against A;Reference number: $40295
A;Accession: $40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-2b chain - mouse
(Species: Mus musculus (house mouse)
(C)Species: Mus musculus (house mouse)
(C)Species: Mus musculus (house mouse)
(C)Species: Mus musculus (house mouse)
(C)Accession: 825057; A02157; A26232; A26233; A35598
(C)Accession: 825057, A02157; A26232; A26233; A35598
(C)Accession: 825057, A02157; A0
                                                                                                                                                                                                                                                                                                                                                           CyGenetics:
A;Map postion: 12
C;Genetics:
A;Map postion: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin G lycoprotein; immunoglobulin; pyroglutamic c;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic c;Keywords: disulfide bond; CH2D region (VDJ)
F;1-117/Domain: Cregion (CH2)
F;118-214/Domain: C1 region (CH2)
F;215-230/Region: hinge
F;215-230/Region: hinge
F;215-230/Region: c2 region (CH2)
F;341-446/Domain: C2 region (CH2)
F;340-427/Domain: G3 region (CH2)
F;350-427/Domain: G3 region (CH3)
F;360-427/Domain: G3 region (CH3)
F;322-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;229,144-199,261-321,367-425/Disulfide bonds: interchain #status predicted
F;229/Disulfide bonds: interchain #status predicted
F;237/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 VHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFCKCPAPNLLGGBSVFIFFPKIKDVLMISLSPWVTCVVVDVSEDPDVQISWFVNNVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%; Score 1415; DB 2; Length 4 58.0%; Pred. No. 1.6e-76; Artive 69; Mismatches 105; Indels
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Matches 268; Conservative
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(domestic sheep)
#text_change 16-Jul-1999
  FPEPVTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASST 230
                                                                                                                                                                  HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 358
                                                                                                                                                                                                     290 EDDFDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKD 349
                                                                                                                                                                                                                                                                            LPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP 418
                                                                                                                                                                                                                                                                                                            ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                     61 ALEWIG-----GSGYDEDIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCAR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TSY-ISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 GQDDPEVQFSWFVDNVEVRTARTKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GPEWVGFIRNKPNGGTTE---YAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 WSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGK 62
                                                            KVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                     SNIKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-
C; Accession: S31459
R; Patri, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A; Reference number: S31459
A; Reference number: S31459
A; Accession: S31459
A; Accession: S31459
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-472 < PAIP
A; Cross-references: EMBL: X69797
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.8%; Score 1429; DB 2; Length 4 Best Local Similarity 58.4%; Pred. No. 2.5e-77; Matches 282; Conservative 63; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-1 chain - sheep (fragment)
C,Species: Ovis orientalis aries, Ovis ammon aries
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C,Accession: $31459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2a chain - mouse
()Species: Mus musculus (house mouse)
()Species: Mus musculus (house mouse)
()Accession: 637483
()Accession: 537483
()Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin P;276-345/Domain: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNT 240
                                                                                                                                                                                                                         63 GPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYI 122
                                                                                                                                                                                                                                                  63 ALEWVGGI---TSGGTTYYNPALKSRLSITKENSK&QVSLSVSSVTPEDIATYYCARS-- 117
                                                                                                                                                                                                                                                                                                                                  123 SHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 182
                                                                                                                                                                                                                                                                                                                                                                                      --TYGEVGDGAIADAWGQGLLVTVSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YISHCRGGVCYGGYFBFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                                                            Gaps
                                                                                                                                              Gaps
                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPUTVTWNSGALKSGVHTFPAVLQSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKV
                                                                                                            WSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGK
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57.3%; Score 1467.5; DB 2; Length
Best Local Similarity 57.7%; Pred. No. 1.3e-79;
Matches 277; Conservative 72; Mismatches 118; Indels
57.7%; Score 1478; DB 2; Length 4 60.9%; Pred. No. 3.1e-80; tive 58; Mismatches 115; Indels
                                                      Conservative
                            Similarity
Query Match
Best Local Simi
Matches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
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Gaps

417

Gaps

19;

58.4%; Score 1494.5; DB 2; Length 444; 60.5%; Pred. No. 3.1e-81; ive 68; Mismatches 95; Indels 19;

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80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWG 139
                                                                                                                                                                                                                                                                                                                                                                   61 KYAESVRGRETISRDDSKSSVYLOMNRLREEDTATYYC-----CRTPWVYA--MDCWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                  140 QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 TPPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 TFPAVLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 ---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 CICTVPEV---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQPSWFVDDVEVHT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
                                                                                                                                                                                                                                                F;251-320/Domain: immunoglobulin homology <IMM>F;22/Disulfide bonds: interchain (to 98) #status predicted F;99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 YSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444
                                                                                                                               Best Local Similarity 60.5%
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S06610
                                                                                                             Query Match
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                    A; Molecule type: DNA
A; Residues: 1-327 <ELL>
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was determined from the germline gene
B; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F)134-203/Domain: immunoglobulin homology <IM2>
F)240-307/Domain: immunoglobulin homology <IM3>
F)240-307/Domain: immunoglobulin homology <IM3>
F)240-307/Domain: immunoglobulin homology <IM3>
F)240-307/Domain: immunoglobulin for light chain) #status experimental
F)27-83.141-201,247-305/Disulfide bonds: #status predicted
F)106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F)17/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLOSS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GLYSLSSWTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.6%; Pred. No. 8.1e-87;
Matches 299; Conservative 12; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%; Score 1586.5; 90.6%; Pred. No. 8.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327
                                                                                                                                                                                                                                                                                                              A)Gene: GDB:IGHG4
A)Cross-references: GDB:119340; OMIM:147130
                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
  Accession: A90933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-470 < &AN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
A;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
MALternates names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (catle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 822080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin; membrane protein
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology < IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 142-470 <SYM>
A,Cross-references: EMBL:X16701
                                                                                                                                                                                                                                                                                                             A; Reference number: $22080
A; Accession: $22080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Remidues: 1-44 <ARA;
C;Comment: This ,catelytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A;Molecule type: protein
A;Mesidues: 238-275 <HOF>
R;Hesidues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
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A; Genetics:
A; Genetics:
A; Genetics:
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C;Genetics:
A; Genetics:
A; Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; MUID:72033500; PMID:4940472
A; Contents: annotation; myeloma protein Sa, disulfide bonds
B; Frangione, B.; Milstein, C.: Pink, J.R.L.
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUID:69064124; PMID:5782707
A; Contents: annotation; Sa, disulfide bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 PSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R, Milstein, C.; Frangione, B.
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Best Local Similarity
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A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-183, 'D', 195-325 < WAN>
A; Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-183, 'D', 195-325 < WAN>
A; Note: Trp-156 is at or near the complement-binding site
B; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino eaid sequences of the three heavy chain constant region domains of a A; Reference number: A90752; WUID:80001357; PMID:113060
A; Contents: myeloma protein Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A) Residues: 1.326 cELL>
A) Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:g6066056
A) Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:g6066056
A) Note: Lys-126 is probably removed posttranslationally
B;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Tmmunol. 125; J048-1054, 1980
A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary and A) Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary and the primary structure of a human IgG2 heavy chain: genetic, evolutionary and the primary structure of a human IgG2 heavy chain: genetic of the primary structure of a human IgG2 heavy chain: genetic of the primary structure of a human IgG2 heavy chain: genetic of the primary structure of the primary structure of the primary structure of a human IgG2 heavy chain: genetic of the primary structure of the primary structure of the primary structure of the primary structure of the primary struc
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Mol. Inmunol. 16, 932-925, 1979
Mol. Immunol. 16, 932-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin A;Tatle: A note on the amino acid sequence of A;Tatle: An ote on the amino acid sequence of A;Tatle: An ote on the Ajalist MUID:80114419; PMID:118920
A;Contente: Zie
A;Accession: A93132
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Species: Homo sapiens (man)
Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
Accession: A93906; A92809; A90752; A93132; A02148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA-------246
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                                                                                                                                                                            47;
                                                                        DB 2; Length 377;
                                                                  Query Match 63.4%; Score 1624.5; DB 2; Length CBest Local Similarity 81.7%; Pred No. 5.46-89; Matches 308; Conservative 10; Mismatches 12; Indels
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                                       Query Match
Best Local Similarity
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Gaps

Length 326;

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Iggamma-3 chain C region (allotype G3m(b)) - human (Species: Homo sapiens (man) (C) Species: Homo sapiens (man) (C) Species: 28-Dec-1987 #text_change 23-Jul-1999 (C) Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999 (C) Accession: A23511 (C) Accession: A23511 (C) Accession: A23511 (C) Accession: A14, 1779-1789, 1986 (C) Action Res. 14, 1779-1789, 1986 (C) Aprile: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con A, Reference number: A23511; MUD: 86148507; PMID: 3081877
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                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
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C,Species: Homo sapiens (man)
C,Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
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A;Status: preliminary
A;Molecule type: DNA
A;Regidues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
P;20-85/Domain: immunoglobulin homology <IMM>
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A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Supperfantly: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin F;20-85/Domain: immunoglobulin homology < IMM>
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R,Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A,Title: A human immunoglobulin IGHG3 allele (GmbO, bl, A,Reference number: A60764; MUID:90007613; PMID:2571587
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63.5%; Score 1626.5; DB 2;
Best Local Similarity 81.7%; Pred. No. 4.1e-89;
Matches 308; Conservative 10; Mismatches 12;
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
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                                                                                               A; Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Note: this sequence has the Glm(17) and Glm(1) markers
A;Note: this sequence has the Glm(17) and Glm(17)
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOI
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-96, R., 99-197, D., 199-238, E', 240, M., 242-266, D', 268-271, D', 273-330 < SCH
A; Residues: 1-96, R., 98-197, D., 199-238, E', 240, M., 242-266, D', 268-271, D', 273-330 < SCH
A; Reall, W.E.; Edelman, G.M.
B; Gall, W.E.; Edelman, G.M.
B; Gall, W.E.; Edelman, G.M.
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: 430565; MUID:71064027; PMID:4923144
A; Fiches: annoctation, disulfide bonds
B; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunogloben bringed cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070267; PMID:1002129
A; Contents: annotation; disulfide bonds
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d 1gM, the subunits associate into la
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F:243-310/Domain: immunoglobulin homology <IM3>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A,Introns: 9911, 1114/1; 224/1.
A,Introns: 9911, 1114/1; 224/1.
A,Introns: 9914, 1114/1; 224/1.
A,Introns: 9914, 1114/1; 224/1.
A,Introns: Department of the submitted from the submitted bain disulfide bonds. In some cases, such as IgA and IgM, the submitts C,Superfamily: immunoglobulin C region; immunoglobulin homology C,Reywords: duplication; glycoprotein; hererotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology < IM12.
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                        MUID:77070269; PMID:826475
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igen Primaerstruktur.
A;Reference number: A91668; WUII
A;Contents: myeloma protein Nie
A;Accession: B91668
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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

March 29, 2003, 09:06:24 ; Search time 21.453 Seconds (without alignments) 2141.995 Million cell updates/sec Run on:

US-09-758-173-8 2561 Title: Perfect score:

1 MGWSLILLFLVAVATRVQCE.......MHEALHNHYTQKSLSLSPGK 478 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	Iq qamma-1 chain C	Ig gamma-3 chain C		chain		monoclonal antibod	Iq heavy chain pre			heavy ch	gamma-		gamma-2b	gamma 2a		gamma 2b chain	gamma	gamma	gamma chain C			heavy chain C	gamma-	qamma-1 chain	qamma-2b chain	gamma-1 c	gamma-3 chain		amma-3 chain
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ALIGNMENTS

RESULT 1
 Ig gamma-1 chain C region - human
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 C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
 K;ELIBSON, U.W.; BERSON, B.J.; HOOG, L.E. Nucleic Acids Res. 10. 4071-4079. 1982.
A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Accession: A93433
 A;Molecule type: DNA
A Residues: 1-330 < ELLA
Although a section is minimally 1/10 allotypic marker. 97-1/vs. and the Glm(1) markers ? AlvOce: this sequence has the Glm(17) allotypic marker.
after translation
Ridaring L.J. Ribmitted to the EMBI. Data Library, October 1000
A:Reference number: S33904
A; Accession: S36861
A; Molecule type: DNA
 A; Residues: 2-330 <har></har>
Kijakanasni, N.; Uedad, S.; Obata, M.; Nikaldo, T.; Nakai, S.; Honjo, T. Cell 29 471.670 1982
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A:reference number: 833887: MITD:83001943: PATH:A:RITING STREET INDITICALIONS FOR EVOLUTION OF A C
A; Accession: S33887
A; Molecule type: DNA
A;Residues: 88-113;235-330 <tak></tak>
 k) Cunningham, B.A.; Kutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.
Distribution of a factor of a home comment of a factor
A;Itte: Ille Covatent Ellicule of a numan gammad-immunoglobulin. VII. Amino acid sequenc A:Reference number: 190563: MITT: 71064074: DMTh. 4400771
A; Contents: myeloma protein Eu
A;Accession: B90563
 A; Molecule type: protein
A; Residues: 1-96, 'R', 98-135 <cun></cun>
A; Note: this sequence has the Gim(3) marker, 97-Arg
Richtelstry 9. 3171-3181. 1970 Bichemistry 9. 3171-3181. 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid semier
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A, Accession: A90564
A Molecule type: protein
A. Kestuduser 136-124, Q. 1156-126, Q. 1167-176, Q. 178-1244, N. 126-129, D. 199-238, E. 240, A. Kestuduser 136-124, D. 189-238, E. 240, A. Nestuduser 136-131, and 341-246
R. Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

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TATAATCAAAAGTTCAAGGGCCGTTTCACTTTATCTCGCGACAACTCCAAAAACACAGGC 1599
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SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/07467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 24,659
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
INPORMATION POR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS: LENGTH: 8120 base pairs TYPE: Nucleic Acid STRANDENBES: Single TOPOLOGY: Linear
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US-09-121-952A-68
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Search completed: April 6, 2003, 06:26:23 Job time : 129.43 secs

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APPLICANT: Geneticch, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: .
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                         AAGGIGGACAAGAAAGIIGAGCCCAAAICIIGIGACAAAACICACACAIGCCCACCGIGC
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COUNTY...
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: D. compatible
CAMPUTER: IEM PC compatible
PC COMPATIBLE PC COMPATIBLE
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Patent No. 6458355
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CITY: South San Fra
STATE: California
COUNTRY: USA
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                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
SOFTWARE: WinPatin (Genentech)
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108
TELECHONE: 650/25-530
TELEPHONE: 650/25-530
TELERPX: 650/952-9881
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS: LENGTH: 8120 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single
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Matches 1257; Conservative
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1945 TCTAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 2004
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                                                                  AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAACTCACACATGCCCACCGTGC
                                                                                                                     GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCCGTGGAGGTGCATAATGCCAAGACA
                                     721 AAGGIGGACAAGAAAGCAGAGCCCAAAICTIGIGACAAAACTCACACATGCCCACCGIGC
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ZIP: 94080
COMPUTER READABLE FORM:
MEDITYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: South San Francisco
STATE: California
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Pred. No. 1.6e-258;
0; Mismatches 159; Indels 21;
                                                                                                                                                                                                                   P1085R3-2
          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REFERENCE/DOCKET NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3·
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.0%;
Best Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                    Linear
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US-09-027-449-68
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Patent No. 6025158
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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US-09-027-449-68
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TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA ; OTHER INFORMATION: referred to as "Molly" US-09-343-485A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC
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                                                                                                                                                                                                                                                                                                                                                Length 18986
                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                             78.5%; Score 1127.4; DB 4; Length 87.8%; Pred. No. 5e-260; tive 0; Mismatches 151; Indels
                            FILE REFERENCE: 037003-0275807
CURRENT APPLICATION NUMBER: US/09/343,485A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/023,715
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 18986
                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                Matches 1262; Conservative
                                                                                                                                                                                                                                                                                                                                                                Similarity
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10129 AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACGTGC 10188
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APPLICANT: Georg, Steven R.
APPLICANT: Deong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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Sequence 2, Application US/09343485A
Patent No. 6413777
GENERAL INFORMATION:
APPLICANT: BEFF, MICHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
                                                                              9949 TICCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCC 10008
                                                                                                                                              10009 TICCCGGCTGTCCTACAGTCCTCAGACTCTACTCCCTCAGCACGCGTGGTGACCGTGCCC 10068
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       9889 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTAC 9948
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US-09-343-485A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1127.4; DB 2; Length
Pred. No. 5e-260;
0; Mismatches 151; Indels
              CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,715
                                                                                                                                                                                                                                                               012712-352
                                                                                STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.8%;
Matches 1262; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
NUMBER OF SEQUENCES:
                                                                CITY: Alexandria
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-09-023-715-2
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TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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78.5%; Score 1127.4; DB 2; Length
Best Local Similarity 87.8%; Pred. No. 5e-260;
Matches 1262; Conservative 0; Mismatches 151; Indels
                                                                                                            ADDRESSE:
CURLES FUNDENNE ADDRESS:
ADDRESSE:
STREET:
STREET:
F.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
Z181: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,866
FILING DATE: 14 MAR.1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELEPHONE: (703) 836-2620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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Sequence 2, Application US/09023715
Patent No. 5998144
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MANMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE S
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                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                PARION AFELICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTONRY, AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                                                                        Floppy disk
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Best Local Similarity 87.8
Matches 1262; Conservative
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Washington
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Patent No. 5830698
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLEAN, Karen Retta
APPLICANT: MCLACHLEAN, Karen Retta
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
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E: PILLSBURY WINTHROP
1100 New York Avenue, N.W., Ninth FL.
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APPLICATION NUMBER: US/08/478,967A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTONEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN INFORMATION:
NAME: TESKIN, ROBIN INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATI
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APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, DIAN E.
APPLICANT: HEOWAN, COLAND A.
APPLICANT: REFF, MITCHELLE R.
APPLICANT: REFF, MITCHELLE R.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
ANTIGEN OF SECURITION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
ANTIGEN OF SECURITION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
ANTIGEN OF SECURITION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
ANTIGEN OF SECURITION ANTIGEN FOR THE TREATMENT OF B CELL
ADDRESSEE: PILLESBERY WINTHROP
ANDERSEE OF SECURITION ANTIGEN FOR THE TREATMENT OF B CELL
ADDRESSEE: ANTIGEN WINTHROP
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661 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 720
3037 TCCAGCAGTTTGGGCACCCAGAACTACATCTGCAAGTGAATCACAAGCCAAGAACAC 3096
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GENERAL INFORMATION:
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3336 1020 3396 1080

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APPLICANT: ANDEANA, National APPLICANT: ANDEANA, National APPLICANT: LEGNARD, John E.
APPLICANT: LEGNARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: RASTETTER, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPBUTIC APPLICATION OF CHIMBRIC AND
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: VITGING ALL
       3157 CCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAACCCAAGGAC 3216
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                                                                                      3217 ACCCTCATGATCTCCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA
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                                                               ACCCTCATGATCTCCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCACGAA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08478967A
Patent No. 5843439
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Pred. No. 4.1e-260;
0; Mismatches 151; Indels 24;
                                                                                                                                                                                                                                           CHROMOSOME/SEGMENT: anti-CD20 in TCAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
TELEFAX. 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.8%;
Matches 1262; Conservative
                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (9
HYPOTHETICAL: NO
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POSITION IN GENOME:
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                                     Score 1127.4; DB 1; Length 9209;
Pred. No. 4.1e-260;
0; Mismatches 151; Indels 24;
                                       Query Match
Best Local Similarity 87.8%;
Matches 1262; Conservative (
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; ANTI-SENSE:
US-08-149-099C-3
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APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Raff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
TITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPOTER: APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FLING DATE: 07-010-1995
CLASSIFICATION: 424
PRIOR APPLICATION UMBER: US 08/149,099
FLING DATE: 03-NOV-1993
PRIOR APPLICATION NUMBER: US 08/149,099
FLING DATE: 03-NOV-1993
ATPOMENTATION NUMBER: US 07/978,891
FLING DATE: 13-NOV-1992
ATTOMENYAGENT INFORMATION:
ANAMER TABLES DESCRIPTION:
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CITY: Alexandria STATE: VA COUNTRY: USA
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Patent No. 5776456
GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
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US-08-149-099C-3
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Sequence 3, Application US/08149099C

Sequence 3, Application US/08149099C

Batent No. 5736137

GENERAL INFORMATION:

APPLICANT: ANDERSON, Darrell R.

APPLICANT: HANNA, Nabil

APPLICANT: HANNA, Nabil

APPLICANT: HANNA, Nabil

APPLICANT: REFF, Mitchell E.

APPLICANT: RASTETTER, Milliam H.

APPLICANT: RASTETTER, Milliam H.

TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND

TITLE OF INVENTION: LYMPHOMA

TITLE OF INVENTION: LYMPHOMA

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: VIGITIA A

COUNTRY: United States

ZIP: 22313-1404
                                                                                                                                                                                   CTCACCGTGGACAAGAGCAGGTGGCAGGAGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: PatentIn Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,099C
FILING DATE: 03.NOV-1993
CLASSIFICATION 18.44
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12.NOV-1992
ATTOMATY AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012/12-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6201
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
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ZUBLE: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITAM PC COMPACTIBLE
COMPUTER: TIMP PC COMPACTIBLE
COMPUTER: TIMP PC COMPACTIBLE
COMPUTER: TIMP PC COMPACTIBLE
COMPUTER: TIMP PC COMPACTIBLE
COMPACE: PATENTIN RATE:
APPLICATION NUMBER: US/08/378,939
FILING DATE: 01-DEC-1992
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTAATION NUMBER: 1808-118
TELEFONGE (202) 783-601
TELEFONGE (203) 783-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1131.8; DB 2;
Pred. No. 2.2e-261;
0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08378939;
Sequence 9, Application US/08378939;
Patent NO. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER;
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES;
CORRESPONDENCES: 46;
CORRESPONDENCE ANDRESS:
ADDRESSE: ROTHWELL, FIGG, ERNST & KURZ
STREET: M.S. THRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.8%;
87.3%;
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Best Local Similarity 87.3°
Matches 1254; Conservative
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LOCATION:
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; LOCATION:
US-08-378-939-9
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US-08-378-939-9
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119 CCTGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTC 178
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                                                                             1246 ACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGGGCAGC
                                                                                                                           1349 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
                                                                                                                                                  1306 AGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACACCACTACACGCAGA
                                                          1289 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFTANTIA SIGNER: C-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1142; DB 1;
Pred. No. 7.7e-264;
0; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08157101A
Patent No. 5808032
GENERAL INFORMATION
APPLICANT: WATSUKURA, TATSUYA
APPLICANT: TSURVORA, NOBUO
APPLICANT: ARINA, KENJI
APPLICANT: ARINA, KENJI
APPLICANT: ARINA, TATSURO
ITILE OF INVENTION: ANTI-HBS ANTIBODY GEN
ITILE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            1409 AGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437
                                                                                                                                                                                                          1366 AGAGCCTCTCCCTGTCTCCGGGTAAATGA 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFENCE/DOCKET NUMBER: 9437/204199
TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
US-08-157-101A-9
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90.8%;
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TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pairs
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Best Local Similarity 90.8<sup>1</sup>
Matches 1249; Conservative
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STRANDEDNESS: single
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US-08-157-101A-9
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                     TATTATATGATGGAAATCAT-----AAATTCTACGCAGACTCCGTGAAGGGCCGATTCA 246
                                                                                                                                    CCATCTCCAGAGATGATTCCAAAAGCATCGCCTATCTGCAAATGAGCAGCCTGAAAATCG 328
                                                                                                                                                                247 CCATTTCCAGAGACAATTCCAAGAACACACTGTATCTGGAAGTGAAGAGCCTGCAAACTG 306
                                                                                                                                                                                                     AGGACACGGCCGTCTATTACTGTACTACATCCTACATTTCACATTGTCGGGGTGGTGTCT 388
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149 ACCACTACATGTATTGGTTCCGCCAGGCTCCAGGGAAGGGGCCGGAATGGGTAGGTTTCA
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Best Local Similarity 90.1
Matches 1270; Conservative
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STRANDEDNESS: single
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                                                                                                                                                             10838 TGA 10840
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                                                                                                                                                                                                      RESULT 3
US-08-157-101A-6
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 9616 GCTCCAGGGCCAGGGGCTGGAGTGCTCACGTATTAGTA-----GTAGTGGTGATCCC 9669
                                                                                                           9817
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                                                               9670 ACATGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAAGAAC 9729
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Patent No. 5808032
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: ATSURUKA, NOBUO
APPLICANT: ATSURUKA, NOBUO
APPLICANT: ATSURUKA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: 9
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
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ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 943:
TELECHONE: 202-861-3711
TELEPHONE: 202-861-3711
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TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
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CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1080
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Best Local Similarity 90.6%; Pred. No. 4.5e-272;
Matches 1307; Conservative 0; Mismatches 92;
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Sequence 3, Application US/09343485A;
Sequence 3, Application US/09343485A;
Patent No. 641377;
GENERAL INFORMATION:
APPLICANT: BARNET, RICHARD S.
APPLICANT: MITCHELL R.
APPLICANT: MICACHIAN, KAREN R.
TITLE OF INVENTION: WEATHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN TITLE OF INVENTION: WAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: WAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: WAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: UNUBER: US/09/343,485A
CURRENT FAPLICATION NUMBER: US/09/343,485A
CURRENT FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-33
PRIOR FILING DATE: 1999-03-34
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE PROFILED NOS: 3
SOFTWARE PROFILED NOS: 3 э; Э 9555 9615 CTCACCGTGGACAAGAGCAGGTGGCAGGAGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 9436 ATGGGTTGGAGCCTCATCTTGCTCTTGTCGCTGTTGCTAGCGGTGTCCTGTCCGAG 9495 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTTACAGCAAG 1320 61 GIGCAACTGGTGGAGTCTGGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120 TGTGCAGTCTCTG----GATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAG 174 Gaps 9 9556 TGCGCAGCCTCCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 1 ATGGGTTGGAGCCTCATCTTGCTTCTTGTCGCTGTTGCTACGCGTGTCCAGTGAG ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTC Description of Artificial Sequence: Synthetic referred to as "Mandy" DB 4; Length 19040; 44; 92; Indels

Sequence Sequence Sequence

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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 1 Sequence 2 Sequence 3 Sequence 4

Sequence 49,

Sequence 8 Sequence 8 Sequence 4

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US-09-315-6978-17

US-08-315-6978-17

US-08-286-740-3

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STRANDEDNESS: not relevant
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INFORMATION POR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN 19.1 AND/OR 87.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACHTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1437;
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REBERENCE/DOCKET UNBER: 35,030
REBERENCE/CONTININER: 35,030
TELEFHONE: 703-836-6620
TELEFRAX: 703-836-6620
                                                                                                                                                                                                                                                       TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS INTITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STREET: 639 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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ALIGNMENTS
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Patent No. 6113898
GENERAL INFORMATION:
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TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 300 -----chaccegesékécriéscecri------ritreaceatresecriés 416 1 ATGGGTTGGAGCCTCATCTTGCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAGG 60 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA TACTCAGACTCAGTGAGGCCGATTCACCATCCAGAGACAACGCCATGAACTCACTG rarcrecaaargaacacccreacacceaegacacaceaegarerrarrarrerereseaca---361 TACATTICACATIGICGGGGTGGTGTCTGCTAIGGAGGTTACTICGAATTCTGGGGCCAG 61 87 121 181 207 261 301 321 378 ઠે 셤 ò В ò g ò g à ద ò qq ઠે g Monoclonal antibody; F protein; respiratory syncytial virus; RSV; Plasmid Glambda-1Bpcd DNA sequence ВР AAC84208 standard; DNA; 1442 (first entry)

19-MAR-2001

AAC84208

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30; Gaps

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The invention provides a human monoclonal antibody (I) and its functional fragments specifically reactive with an F protein epitope of respiratory syncytial virus (RSV), and capable of neutralizing infection by the virus such as Glambda-1A or Glambda-1B. The antibody can be expressed by standard recombinant methodology. (I) is useful for detecting RSV by contacting a source suspected of containing RSV with (I) and determining whether (I) binds to the source. (I) is also useful for providing passive immunotherapy prophylactically, to RSV disease in a human. (I) is useful for therapeutic and/or prophylactic treatment of RSV infection in human patients, particularly infants and young children. (I) is also useful as a diagnostic reagent for the determination of RSV mediated disorders or for tracking progress of treatment of the disorders sequence represents the continuous DNA sequence of the coding region of the heavy chain of plasmid Glambda-1Bpcd.
                                                                                                                                                                                                                                                                                                                                                                       therapeutic and/or prophylactic treatment of respiratory syncytial virus infection, is specifically reactive with the F protein epitope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1169.4; DB 22; Length 1442;
Pred. No. 3.1e-224;
0; Mismatches 111; Indels 30;
                                                                                                                                                                                                                                                                                                                                                        Human monoclonal antibody and functional fragments, useful for
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human; virucide; RSV propagation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3, 6; Fig 10A-B; 102pp; English.
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Best Local Similarity 90.2<sup>3</sup>
Matches 1296; Conservative
                                                                                                                                                                                                                                                                           Sweet RW,
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                                                                            WO200069462-A1
                                       Homo sapiens
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Glambda-1;
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             GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACA
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respiratory syncytial virus; complementarity determining region; CDR; infection; immunotherapy; therapy; diagnosis; Hu19BHcpcd; ss. Plasmid Hu19BHcpcd encoding anti-RSV F protein Hu19B heavy chain. Monoclonal antibody; human; Hu19B; engineered antibody; RSV; HB. AAV41429 standard; DNA; 1427 12-OCT-1998 (first entry) AAV41429; RESULT 14

Location/Qualifiers Homo sapiens

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480

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306 360

WO9819704-A1

14-MAY-1998

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This is the DNA sequence of plasmid Hu19BHcpcd, which includes a coding region for anti-respiratory syncytial virus (RSV) fusion (F) protein human monoclonal antibody (MAD) Hu19B heavy chain (see also AAW59616). Hu19BLcpcn (see AAV41430) encoding the Hu19B light chain is also provided. These vectors were used to produce Hu19B in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19B in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19B in transfected from 19A, 19B, 19C or 19D (see AAW59615-18); a light chain selected from 19A, 19B, 19C or 19D (see AAW59615-18). These are neutralising engineered antibodies that inhibit virus crowth in vitro and in vivo in animal models of RSV infection. They can be used in the detection, prevention and passive immunotherapy of RSV infection. Nucleic acids encoding the human combinant plasmids (see AAV41427-33) and host cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GTGCAGCTGGTGGAGTCTGGGGGGAGGCCTGGTCAGGCCTGGCGGGTCCCTAAGACTCTCG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCCAGAGATGATTCCAAAAGCATCGCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TGEGAGCCTCTGGAACCACCCTCAGTGGCTATACCATGCACTGGGTCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGGTTGGAGCCTCATCTTGCTCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 TACTCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTT
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                                                                                                                                                                                                                                  Monoclonal antibodies reactive with Respiratory Syncytial Virus useful for detection, prevention and treatment of RSV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1169.8; DB 19; Length 1427; Pred. No. 2.5e-224;
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                                                                                                                               Sweet RW;
                                                                                                                                                                                                                                                                                                 Example B; Fig 4C; 109pp; English
                                                                                                                             Porter TG,
                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                          P-PSDB; AAW59625 and AAW59628
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                                          96US-0030149.
97WO-US19203
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                                                                                                                                                                     WPI; 1998-286600/25
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  23-OCT-1997;
                                          01-NOV-1996;
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                  1003 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGGTCTCCAACAACAAGAGCCCTCCCA
                                                                 GCCCCCATCGAGAAAACCATCTCCAAAAGCCAAAAGGCCCCCGAGAACCACAGGTGTAC
                                                                                        GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAAGGCAGCCCCGAGAACCACAGGTGTAC
                                                                                                                                               Monoclonal antibody; human; Hu19D; engineered antibody; RSV; respiratory syncytial virus; complementarity determining region; CDR; infection; immunotherapy; therapy; diagnosis; Hu19DHcpcd; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid Hu19DHcpcd encoding anti-RSV F protein Hu19D heavy chain.
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"alters codon AAC (Asn)
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P-PSDB; AAW59625, AAW59628 and AAW59632.
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coding region for anti-respiratory syncytial virus (RSV) fusion (F) protein human monoclonal antibody (MAb) Hu19D heavy chain (see also AAW55618). Hu19CLCpcn (see AAV41413) encoding the Hu19C light chain is also provided. These vectors were used to produce Hu19C in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19D MAbs are claimed. These are reshaped human antibodies comprising a heavy chain selected from 19A, 19B, 19C or 19D (see AAW55615-18), and a light chain selected from 19A, 19B, 19C or 19D (see AAW55620-21). These are neutralising engineered antibodies that inhibit virus growth in vitro and in vivo in animal models of RSV infection. They can be used in the detection, prevention and passive immunotherapy of RSV infection. Nucleic acids encoding the human MAbs, recombinant plasmids (see AAV41427-33) and host cells are
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                                                   This is the DNA sequence of plasmid Hul9DHcpcd, which includes a
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Pred. No. 1.2e-224;
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C; Fig 4F; 109pp; English.
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Best Local Similarity 89.8%;
Matches 1291; Conservative
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10713 AGCAAGCTCACCGTGGACAAGAGCAGGGGGGACGAGCAGCTCTTCTCATGCTCCGGG 10772
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                                    1375 ATGCATGAGGCTCTGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibodies reactive with Respiratory Syncytial Virus .
useful for detection, prevention and treatment of RSV infections
                                                                                                                                                                                                                                               Plasmid Hu19CHcpcd encoding anti-RSV F protein Hu19C heavy chain.
                                                                                                                                                                                                                                                                      Monoclonal antibody; human; Hu19C; engineered antibody; RSV; respiratory syncytial virus; complementarity determining region; CDR; infection; immunotherapy; therapy; diagnosis; Hu19CHcpcd; s
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                                                                          30;
Score 1171.4; DB 19; Lengt
Pred. No. 1.2e-224;
0; Mismatches 116; Indels
   81.5%;
           Query Match
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Reff ME Barnett RS, McLachlan KR, WPI; 1998-521229/44.

9 Site specific integration of DNA in mammals for expressing, immunoglobulins - comprises homologous recombination using selectable marker and target plasmids.

Example 1; Fig 10; 114pp; English

This is the nuclectide sequence of novel target plasmid Mandy. The plasmid includes an inactivated murine dihydrofolate reductase. (DHFR) gene, the Escherichia coli beta-galactorsidase gene, baculovirus DNA, a cassette comprising the promoter and enhancer elements from cytomegalovirus and Sv40 virus, the E. coli hactivated Salmonella typhimurium histidinol dehydrogenase (Hisp) gene and transposon TnS neemycin phosphotransferase (meo) gene end mammalian cell with a 'marker plasmid' such as Desmond (see ANA67792), which cell with a 'marker plasmid' such as Desmond (see ANA67792), which contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination with the unique sequence which provides for homologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene es of the end of the marker plasmid into the mammalian cells. Exons I and commologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene and ecombination of the marker plasmid into the mammalian cells. Exons I and 2 are present on the marker plasmid into the mammalian cells. Exons I and 2 are present on the marker plasmid into the mammalian cells. Exons I and 2 are present on the mammalian cells. Exons I and 2 are present on the mammalian cells of the marker plasmid into the mammalian cells. Exons I and 2 are present on the mammalian cells of the marker plasmid into the mammalian cells of a riphly spliced delect

Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;

٠, ش 45; Gaps 82.3%; Score 1182.2; DB 19; Length 19035; 90.8%; Pred. No. 1.1e-226; Live 0; Mismatches 88; Indels 45; G Best Local Similarity 90.8 Matches 1310; Conservative Query Match

- 9432 AricGarricGAGCCTCATCTTGCTCTTGTCGCTGTTGCTACGCGTGTCCTGTCCGAG 9491 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120 1 AIGGGIIGGAGCCTCAICTIGCTCTICCTIGITGCTACGCGGGTCTCCAGTGAG 60 61 ઠે 음 ઠે
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9993 CACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC 10052 10532 10172 10352 10472 10112 10233 AAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC 10292 CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCACCG 10652 GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGCCTCCTTCTTCTTCTTAC 10712 1014 1134 9666 ACATGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAAACGCCAAGAAC 9725 9872 9932 9992 654 714 774 1315 AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 1374 474 534 594 834 954 235 ACAGAATACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGC 294 295 ATCGCCTATCTGCAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTACT 9726 ACACTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG 9813 GGCCAGGGAGTCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACCTGC 355 ACATCCTACATTTCACATTGTCGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTCTGG 9786 A-----GCTTGACTACAGGGTCTGACTCCTGG 9873 CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG 10053 GIGCCCTCCAGCAGCTIGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGC CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCC AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACC GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGAGCCCCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTAC 415 GGCCAGGGCCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGCCTGGTCAAG 535 GACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTG 595 CACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGC AACACCAAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA 10113 AACACCAAGGTGGACAAGAAGTTGAGCCCAAATCTTGTGAAAACTCACACAGGCCCA CTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAAGGGCAGCCCCGAGAACCACAG AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCCGTGGAGGTGCATAATGCC GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGC CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG 475 655 715 775 835 895 955 1075 10533 1195 10473 10293 10353 1015 10413 1135 10593 1255 g g 유 ò ò ద ò 셤 ò ద ò g ò qq ò a 셤 ò g ò 셤 g ò g 임 g ò à ò ð ò ò 셤 ò ò

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homologous recombination; vector; neomycin phosphotransferase;
neo gene; selectable marker; immunoglobulin; CD23; 5E8; human;
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                                                                                                                Traget plasmid Mandy containing anti-CD23 gene.
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Chimeric - Baculovirus.
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Chimeric - Rhesus macaque polyoma virus.
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Chimeric - Photinus sp.
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Pred. No. 6e-227;
0; Mismatches 135; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
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P-PSDB; AAR20057.
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ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allersy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, czema, hasmophilia, thrombosis, The present sequence encodes a protein of the invention.
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                                                                                                                                                            82.4%; Score 1184; DB 22; Length 1644; 90.3%; Pred. No. 3.8e-227; ive 0; Mismatches 130; Indels 9;
                                                                                                                                   Sequence 1644 BP; 382 A; 509 C; 453 G; 300 T; 0 other;
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Matches 1301; Conservative
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the primers, for sequencing, for chromosome or gene mapping, in the primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to target antibodies/lelicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. 1320 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 1312 CTCACCGTGGACAAGAGCAGCAGCAGCAGCAGCAGCATCTTCTCATGCTCCGTGATGCAT 1371 Human; novel protein; 88; Antianaemic; osteopathic; antiinflammatory; Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAAC AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTACAGCAAG Human cDNA encoding a novel human protein #159. Claim 1; Page 387-389; 894pp; English. ВР AAS22593 standard; cDNA; 1644 RT; 25-JAN-2001; 2001WO-US02623 25-JAN-2000; 2000US-0491404 (first entry) Fang YT, Liu C, Drmanac WPI; 2001-451939/48. (HYSE-) HYSEQ INC P-PSDB; AAU14288 WO200155437-A2 24-OCT-2001 Homo sapiens 02-AUG-2001. AAS22593; 1192 1261 1252 1201 1321 g g g ò ઠે ò ò 8

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This polynucleotide sequence represents the cDNA of the heavy chain of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rabies virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimmeric immunoglobulin light chain and a fused gene encoding a chimmeric immunoglobulin. The antibody of the invention is useful for treating an individual exposed to a rabies virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post exposure prophylactic therapy for individuals exposed to a rabies virus.
                                                                                                                                                                                                                      HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain; human monoclonal rabies virus neutralising antibody; immunoglobulin; light chain; central nervous system; CNS; prophylactic therapy; clone JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120
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1511 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCYCCGGGTAAATGA 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated human monoclonal rabies virus neutralising antibody useful for treating individual exposed to rabies virus and for preventing spread of rabies virus to central nervous system -
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                                                                                                                                                                                        cDNA of the heavy chain of the monoclonal antibody from clone JA
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Pred. No. 2.4e-227;
0; Mismatches 130; Indels 12;
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/product= "JA clone heavy chain protein"
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